

BEST AVAILABLE COPY



MAJORITY	ATGXXGGCGATGCTTCCCTCTCTTTGAGCCCCAAAGGCCGGGTCTCTCTGGTGACGGGCACCCACCTGGCCT	
DNAPTAQ	...AG..G.....G.....G.....	70
DNAPTFLC..G.....	67
DNAPTTH	...GA.....G.....A.....	70
MAJORITY	ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCCACCCOGGGGGGAACCGGTGCAGGGGCTCTACGGCTT	
DNAPTAQCA.....G.....G.....	140
DNAPTFLT.....C.....C.....C..T.....	137
DNAPTTHG.....G.....	140
MAJORITY	CGCCAAGAGCCTCTCAAGGCCCTGAAGGAGGACGGGGACXXGCCGGTGXTCGTGCTTTGACGCCAAG	
DNAPTAQC.....C.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	280
MAJORITY	GCCCCCTCCTTCGGCCACGAGGCCTACGAGGCCCTACAAGGGGGGGCCCCACCCCCGGAGGACTTTC	
DNAPTAQG..GG.....G.....	277
DNAPTFL	274
DNAPTTHGA.....G.....C.....	280
MAJORITY	CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGACCTCCTGGGGCTTGCGCGCCTCGAGGGTCCCCCGGCTA	
DNAPTAQA.....G.....G.....	347
DNAPTFLG.....T.....A..C.....T...G..G.....T.....	344
DNAPTTHT.....T..A..C.....	350

FIG. 1A

MAJORITY	CGAGGCGGACGACGTXCTGGCCACCCTGGCCCAAGAGGCGGAAAGGAGGGGTACGAGGTGCGGCATCCTC	
DNAPTAQC.....G.....C.....C.....	417
DNAPTFL	T.....G.....CG.....	414
DNAPTTHT..C.....	420
MAJORITY	ACCGCCGACCGGACCTCTACCAGCTCCTTTCCGACCCGCATCGCCGTCTCCACCCCGAGGGGTACCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G.....G.....A.....T.....G.....	484
DNAPTTHA..G.C.....G.....CC.....	490
MAJORITY	TCACCCCGGCGTGGCTTTGGGAGAGAGTACGGCCTGAGGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC	
DNAPTAQC.....A.....C..C.....CC.....A..	557
DNAPTFLAC.....C.C.....T..C.....C.T	554
DNAPTTHA.....C.....	560
MAJORITY	GGGGGACCCCTCCGACAACCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG	
DNAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFLG..T...A.....G.....A..G...A..CGC	624
DNAPTTHTC.....A..	630
MAJORITY	GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAAGCCCGC...CXTCCGGGAGAGAAG	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..C..C.....A.....T....T.G.....C	691
DNAPTTHA.....A.....A.AAAA.G.....	700

FIG. 1B

FIG. 1C

FIG. 1C

MAJORITY CGGGGXCTCCTCGCCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGGGCTXGACCTCXTGCCCCGGGGACG
 DNAPTAQG..T.....A.....AG.....C.....A.....T.G.....CC.....C..... 1114
 DNAPTFLAA.....G.....G.....C.....G.....T.C..A.A..... 1111
 DNAPTTHC.....C.....C.....TC.....G..A.....G..... 1120
 MAJORITY ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACACCACCCCGAGGGGTGGCCCGCGCTACGG
 DNAPTAQT.....T.....T.....T.....T.....T.....T..... 1184
 DNAPTFLG.....T.....T.....T.....T.....T.....T..... 1181
 DNAPTTHT.....T.....T.....T.....T.....T.....T..... 1190
 MAJORITY GGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG
 DNAPTAQ C.....G.....G.....GC.....T.....G.....GCC.....GTG..G. 1254
 DNAPTFLT.....A.....A.....GG.....C.C.....A..C...AAA.... 1260
 DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260
 MAJORITY CGCCTTGAGGGGAGGAGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAGCCCCCTTTCCCGGGTCCIGG
 DNAPTAQ A.G.....G.....G.....G.....G.....GCT..... 1324
 DNAPTFLA...A..A..AC.C..G.....G.....G.....GT... 1321
 DNAPTTHC.....A.....C.....C.....A.....C..... 1330
 MAJORITY CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA
 DNAPTAQG..C.....G..C.....T...AG.....T.G.....C... 1394
 DNAPTFLGG.....C.....C.....C.....A..C 1391
 DNAPTTHC.....A.....A.....T.....T.....C.T..... 1400

FIG. 1D

MAJORITY	GGAGATCCGCCGCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCCGGGAC	
DNAPTAQGC.....CC.....	1464
DNAPTFLG.G....AG..G.....	1461
DNAPTTHT.....G.....	1470
MAJORITY	CAGCTGGAAAGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC	
DNAPTAQC.....A.....	1534
DNAPTFLGC.....G.C..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....	1540
MAJORITY	GCTCCACCAGCGCCGCTGCTGGAGGCCCTXCGXGAGGCCACCCCATCTCGTGGAGAAGATCCTGCAGTA	
DNAPTAQC.....C..C.....	1604
DNAPTFLT.....G..A.....CCGC.....	1601
DNAPTTHG.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCCCTGCCXGXCCTCGTCCACCCCAAGGACGGGC	
DNAPTAQG....G.....T.....T....G.A....A.....	1674
DNAPTFLA.....A.....C.C..G.....A...C...	1671
DNAPTTHG.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGGCACGGGACGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQA.....A.....T.....C..	1744
DNAPTFLG.....C.....TCC.....	1741
DNAPTTHG.....G.....	1750

FIG. 1E

MAJORITY AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCGGGCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAQG..T..G.....A.C.....G...C. 1814
 DNAPTFLG.....C.C.....A.....C.... 1811
 DNAPTTHCT.....C...T....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ A.....A.....A...G.....C..... 1884
 DNAPTFL .C.....T.T.....C.....T..... 1881
 DNAPTTHC.....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCCGACGCTGGATGTTCCGGCGTCCCCCGG

DNAPTAQC.....C.....GG.....G... 1954
 DNAPTFLT.....T.....TT....C. 1951
 DNAPTTH ...A.....A.....A..... 1960

MAJORITY AGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCGGC

DNAPTAQA.....G... 2024
 DNAPTFL .A.GG..A....T.....G..... 2021
 DNAPTTHGG.G.....C..... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCCATCCCCCTACGAGGAGGCGGTGGCCCTTCATTGAGCGCTACTTCCAG

DNAPTAQA.....T.....CCA.....T... 2094
 DNAPTFLGG.....T..... 2091
 DNAPTTH ...TA.G.....T..A.....A 2100

FIG. 1F

MAJORITY	AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGCGGGGGTACGTGGAGA	
DNAPTAQ	2164
DNAPTFL	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTHA.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTCGGCCGCGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA	
DNAPTAQC.....A.....AG.G.....C..	2234
DNAPTFLT.....C.....	2231
DNAPTTH	...AA.AA.....CA.....C.....	2240
MAJORITY	GCGCATGGCCCTTCAACATGCCCCGTCCAGGGCACCCGCCGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQT.....T.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCTCCTXCAGGTCCACGACGAGCTGGTCCTCGAGGCC	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTHC..C.G...G.....C.C.....CC.....G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCCCGCTTTGGCCAAGGAGGTTCATGGAGGGGGTCTATCCCCCTGGCCGT	
DNAPTAQ	.A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	...G..C.....AG...A.....GG.....CAG..	2441
DNAPTTH	.C...C.....C...A.....G.....C.....AA..C.....C.....	2450

FIG. 1G

MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQA.....GA	2499
DNAPTFLCC.....	2496
DNAPTTHT.....GT...	2505

FIG. 1H

MAJORITY MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVVFDK

 TAD PRO .RG.....H.....I..... 69
 TFL PROV.V..... 68
 TTH PRO .E.....YK..F..... 70

 MAJORITY APSFRHEAYEAYKAGRAPTEDFPROLALIKELVDLLGLXRLEVPGEADDVLATLAKAEKEGYEVRIL

 TAG PROGG.....A.....S..... 139
 TFL PROV.....F.....R..... 138
 TTH PROFT..... 140

 MAJORITY TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDNLPGVKGIGECTAXKLLX

 TAG PRO ...K.....H.....D.A...T.E.....R...E 209
 TFL PROE..I.....Y.....A...I.....QR..IR 208
 TTH PROV...V.....H...E.....F...V.....L...K 210

 MAJORITY EWGSLNLLKNLDRVKP·XXREKIXAHMEDLXLSSXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF

 TAG PROA.....L...AI...L...D..K..WD..AK.....K.....R..... 278
 TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL..... 277
 TTH PROENV.....K..L...R..LE..R.....L.QG..... 280

 MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV

 TAG PROS.....K.....D.....PE.YKA.....A 348
 TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G. 347
 TTH PROA.AP.....K.....C.D.....A...A..K..... 350

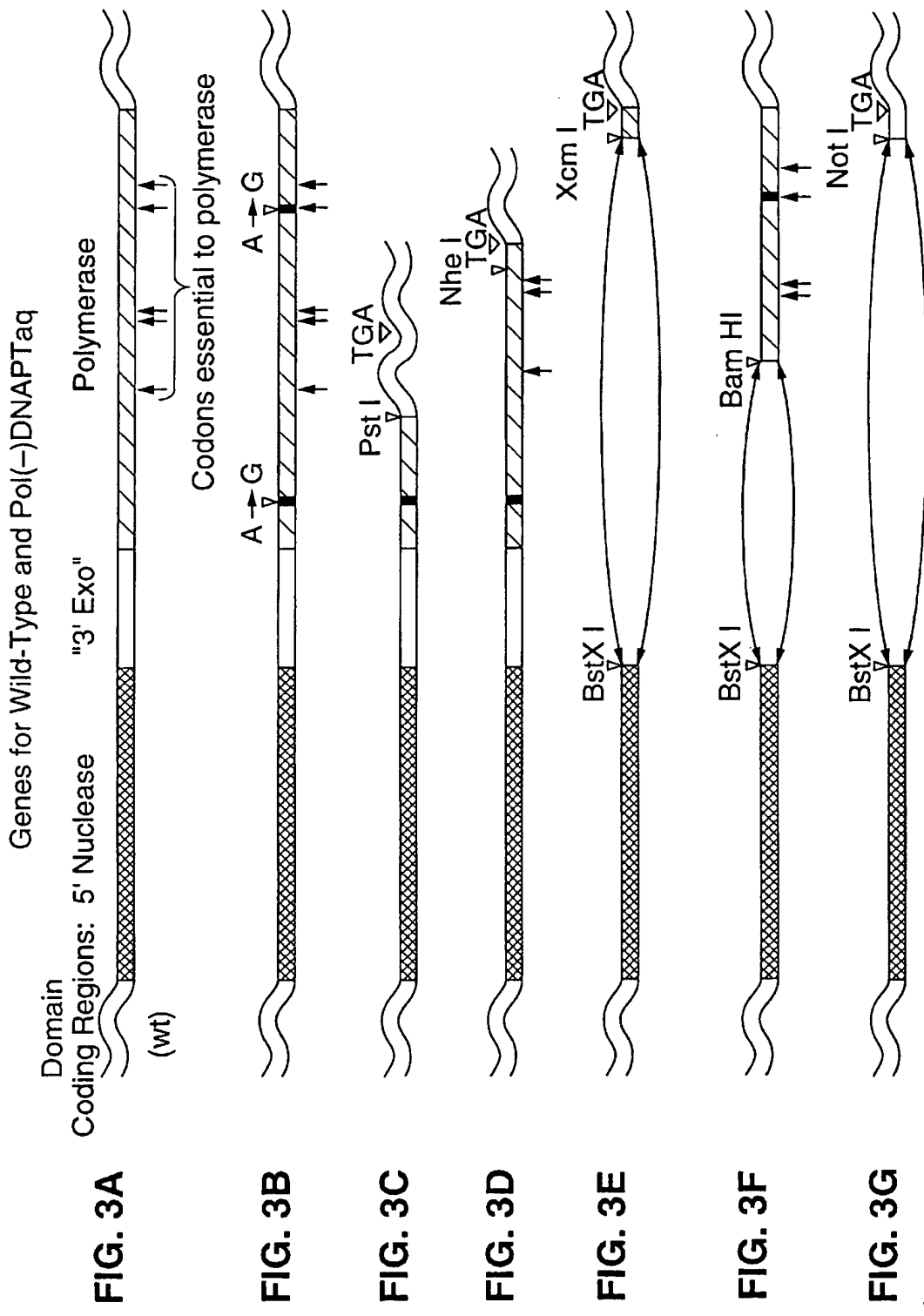
FIG. 2A

MAJORITY	RGLLAKDLAVLALREGDLXP	GDDPMLLAYLLDPSNTT	PEGVARRYGG	EWTE	DAGERALLSERLFXNLXX	
TAQ PROS.....	G.P.....E.....	A.....A.....	A..WG	418
TFL PROI.....	F.E.....A.....QT..KE		417
TTH PROS.....	V.....AH.....HR..LK		420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEE	IRRL	EEEE	VFRLAGHPFNLNSRD		
TAQ PROR...R...A.....R.....A...A.....			488
TFL PROK.....E.....R.....EA.V.Q.....			487
TTH PROK.....H.....L.....				490
MAJORITY	QLERVLFDELGLPAIGKTEKTKRSTSA	AAVLEALREAHPIVEKILQYRELTKL	KNTYIDPLPXLVHPRTG			
TAQ PROR.....S.....D.I.....			558
TFL PROR.....DR.....A...K...			557
TTH PROR..L...Q.....H.....V...S.....			560
MAJORITY	RLHTRFNQTATATGR	LSSDPNLQNI	PVRTPLGQRIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL			
TAQ PROI.....L.....				628
TFL PROV.....V.V.....				627
TTH PROA.....A.A.....				630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHL	SQELAI	PYEEA	VAFIERYFQ		
TAQ PROE.....R.....Q.....				698
TFL PROS..G.....G..S.....				697
TTH PROK.....V.....					700

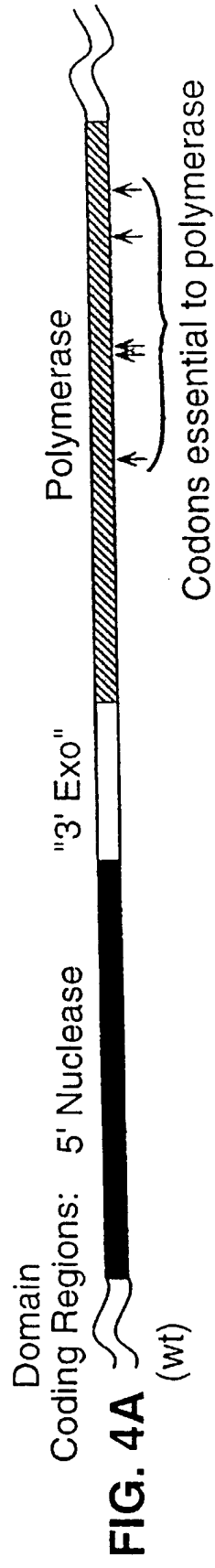
FIG. 2B

MAJORITY	SFPKVR	AWIEKT	LEEGRR	RGYVET	LFGR	RRYVP	DLNAR	VKS	VREA	ERMA	FNPV	QGT	AADL	MKL	AMV	KL	
TAQ PRO	E.....	768
TFL PRO	767
TTH PRO	770
MAJORITY	FPRLX	EMGAR	MLLQ	VHDEL	VLEAP	KXRA	EXVA	ALAKE	VM	EGVY	PLAV	PLEV	EV	GXG	EDW	LSA	KEX
TAQ PRO	E.....	A.....	R.....	833
TFL PRO	831
TTH PRO	835

FIG. 2C



Genes for Wild-Type and Pol(-)DNAPTfl



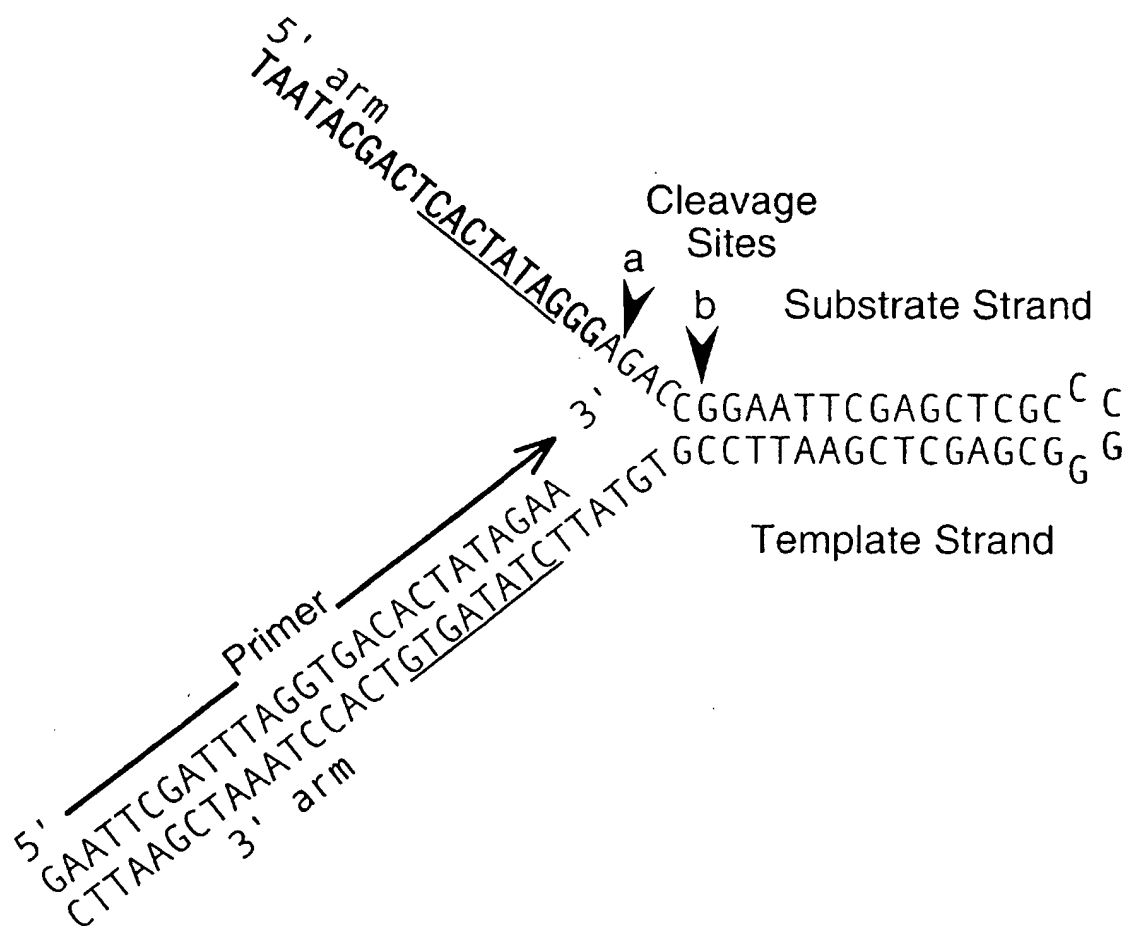


FIG. 5

DNAP
TARGET
DNA

	T		S		
	┌───┐		┌───┐		
M	-	+	-	+	M

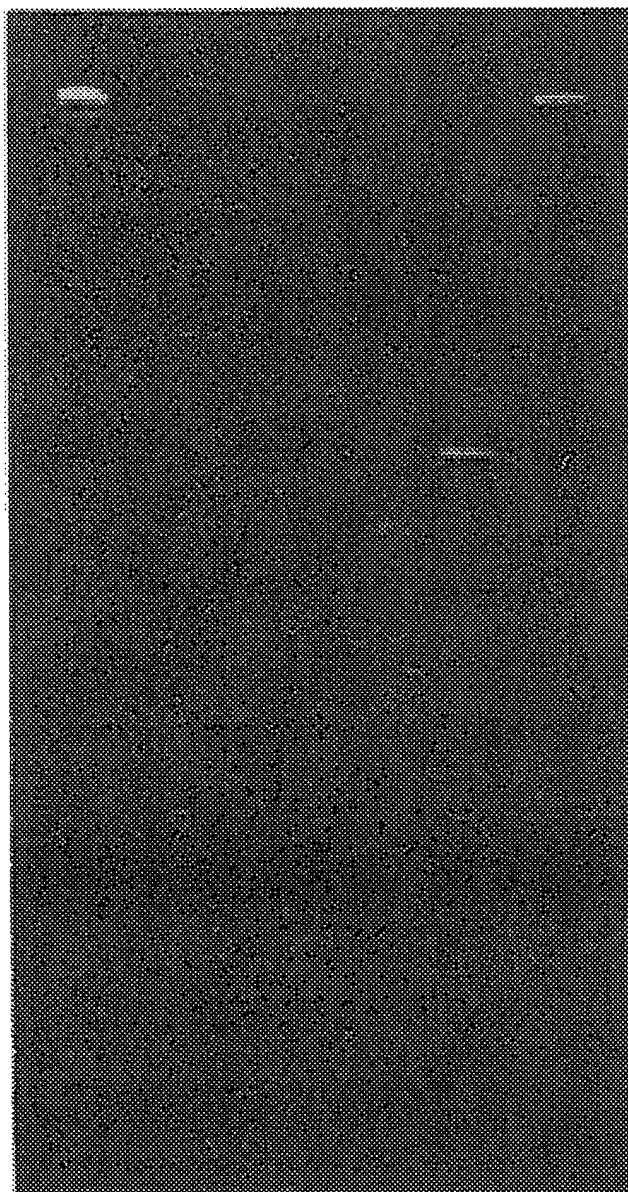


FIG. 6

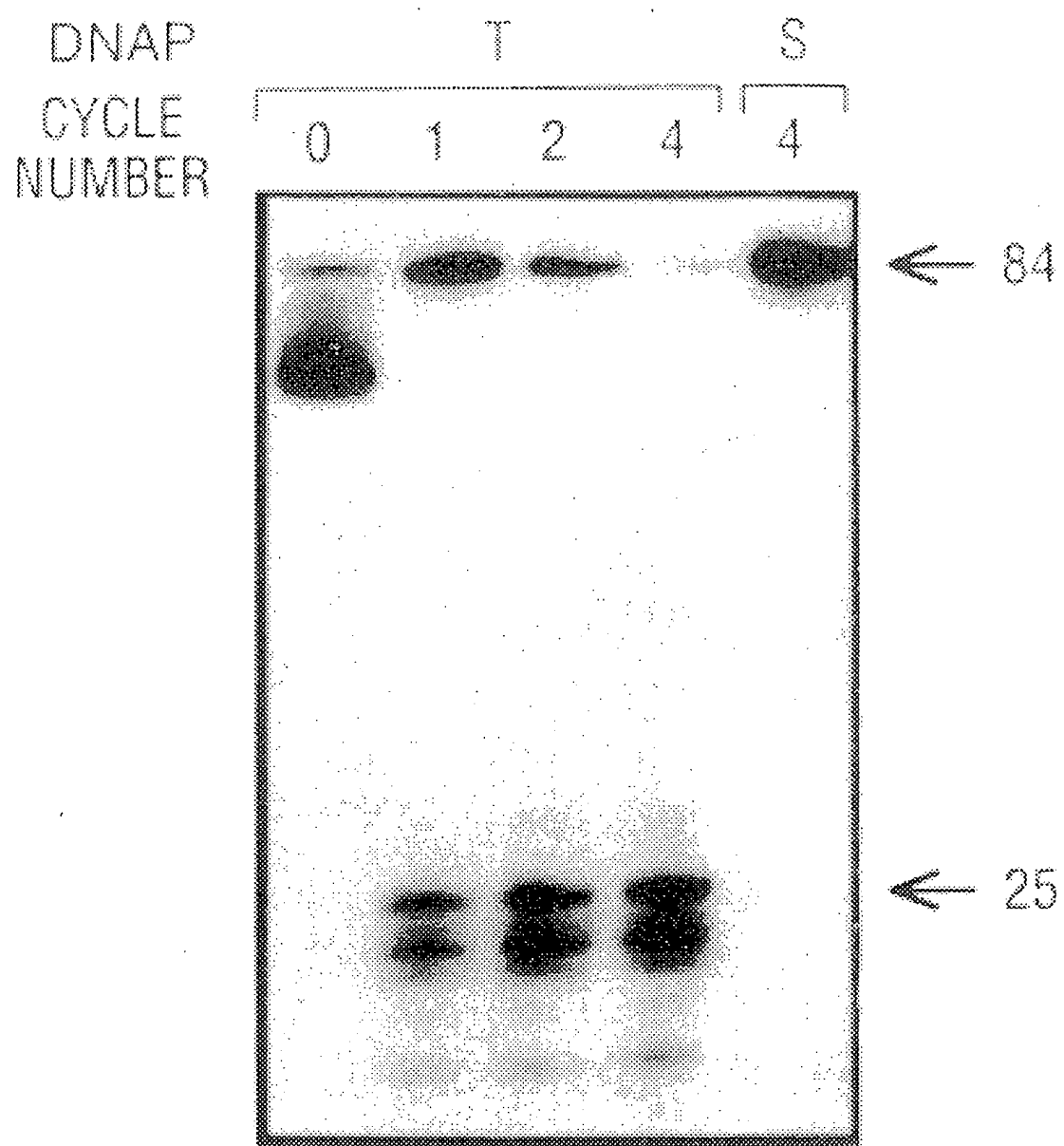


FIG. 7

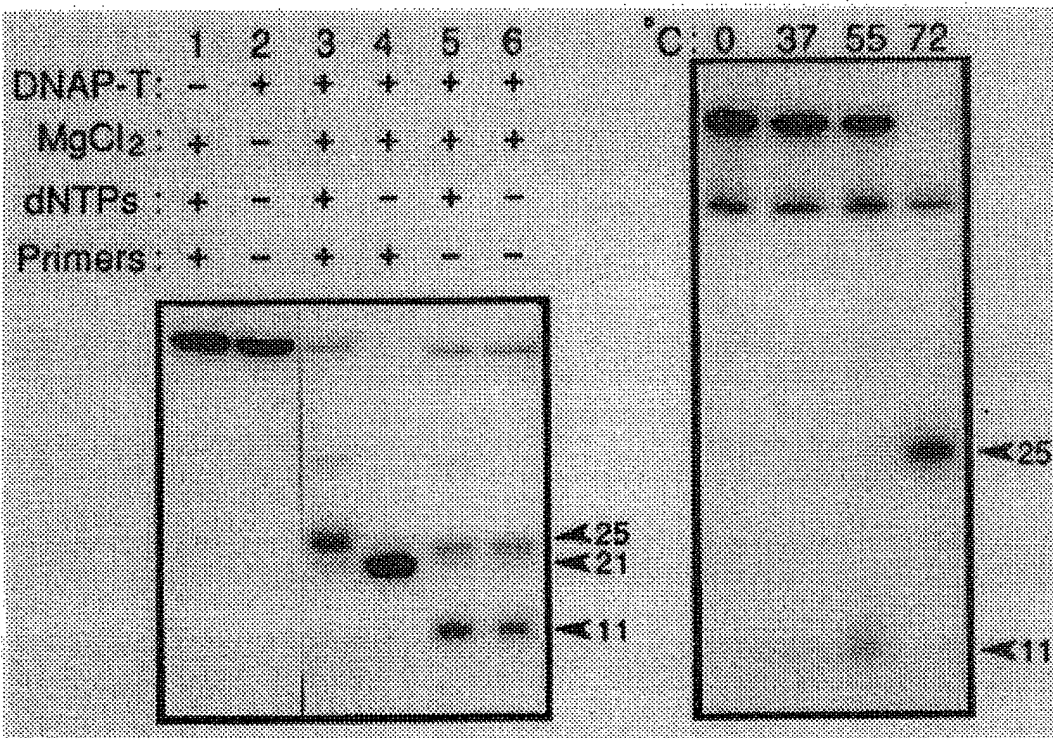


FIG. 8A

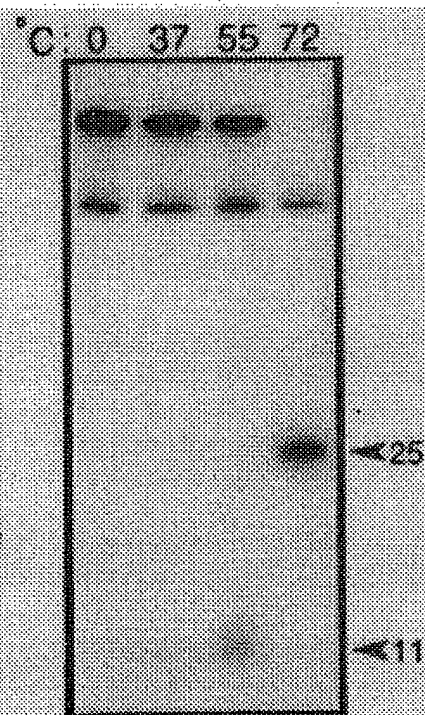


FIG. 8B

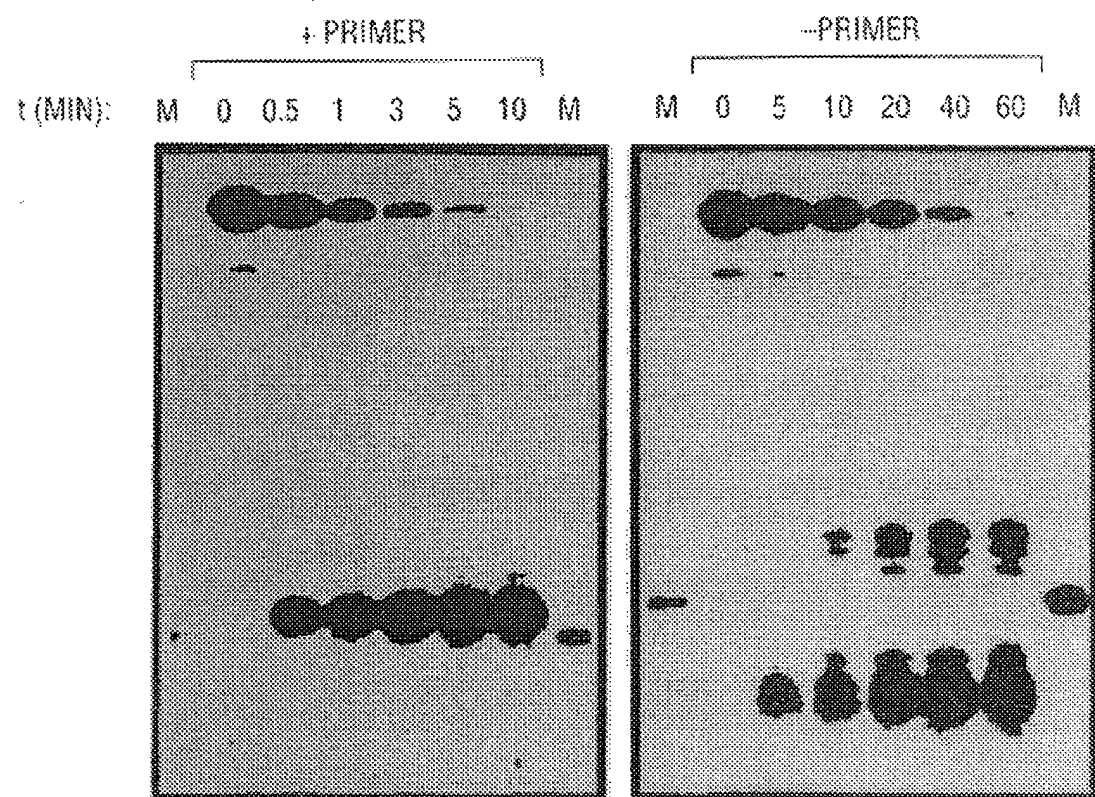
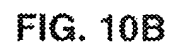


FIG. 9A

FIG. 9B



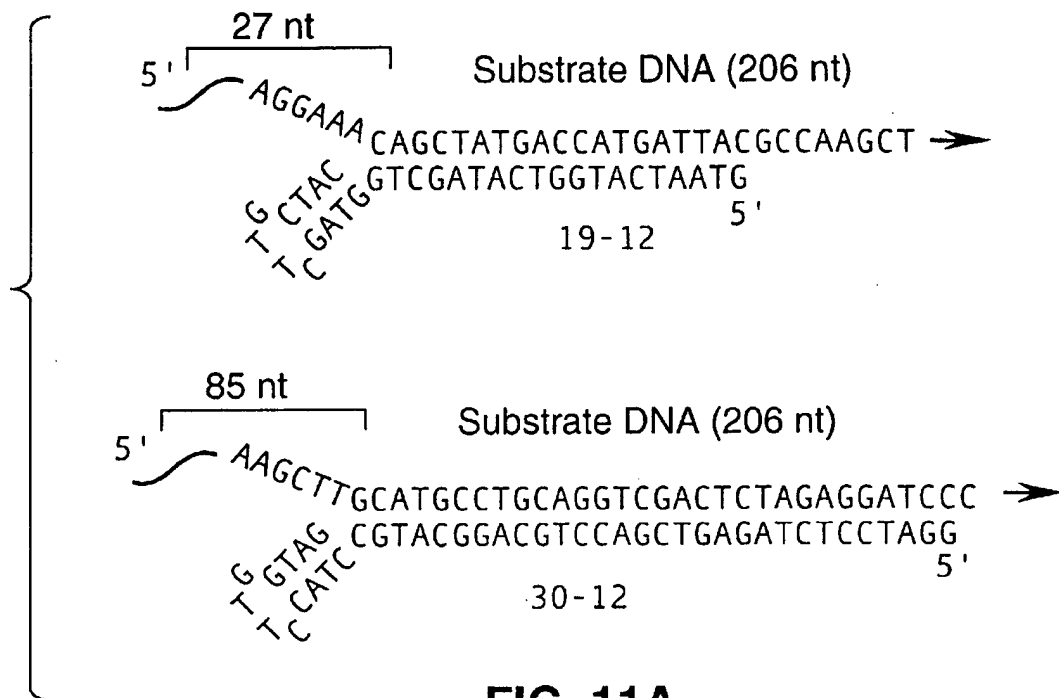


FIG. 11A

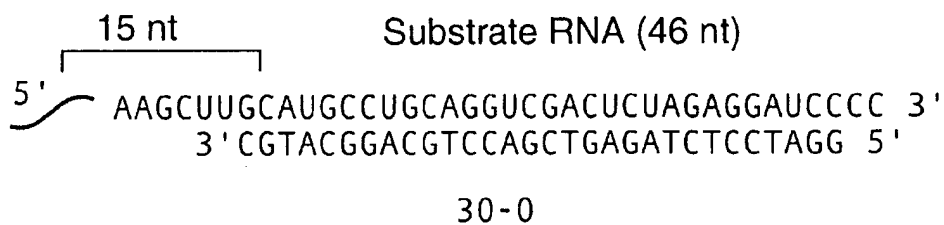


FIG. 12A

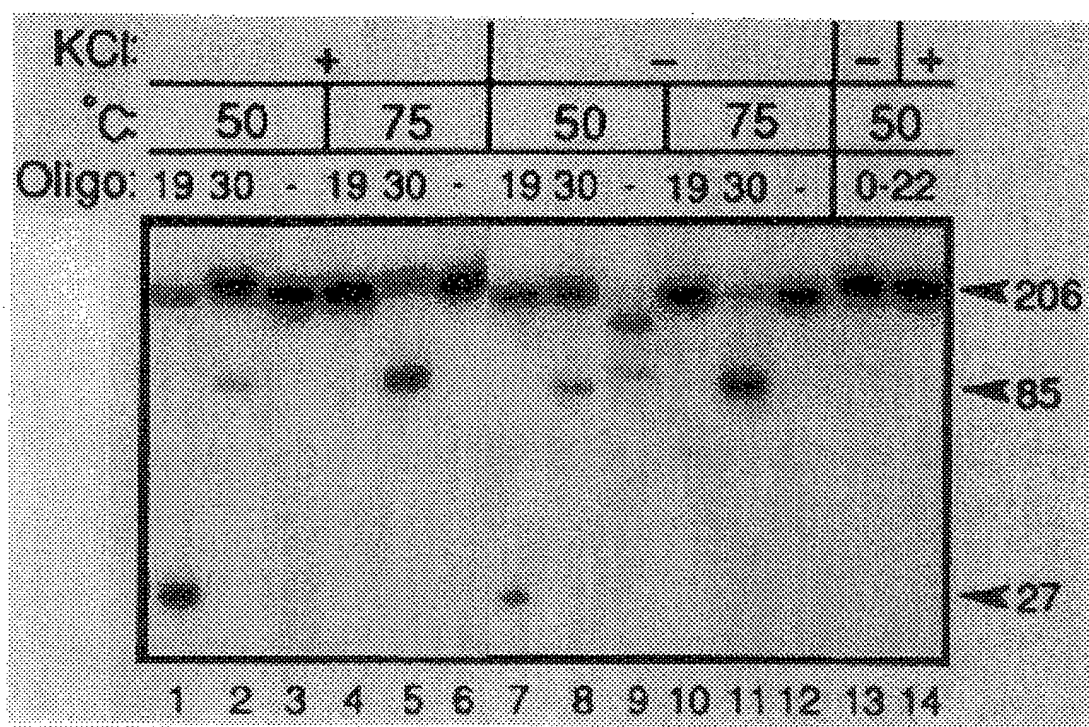


FIG. 11B

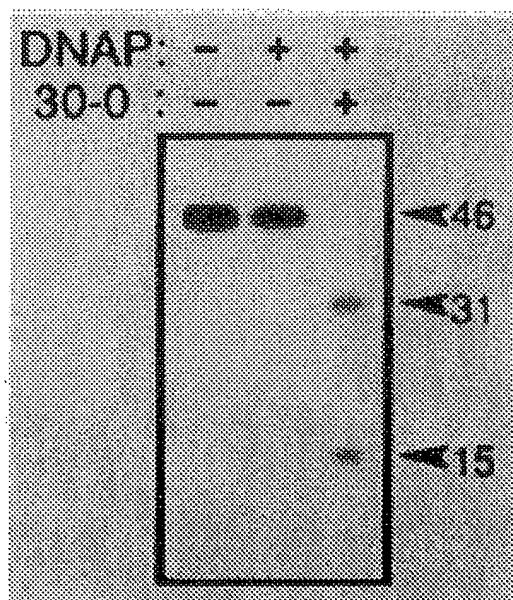
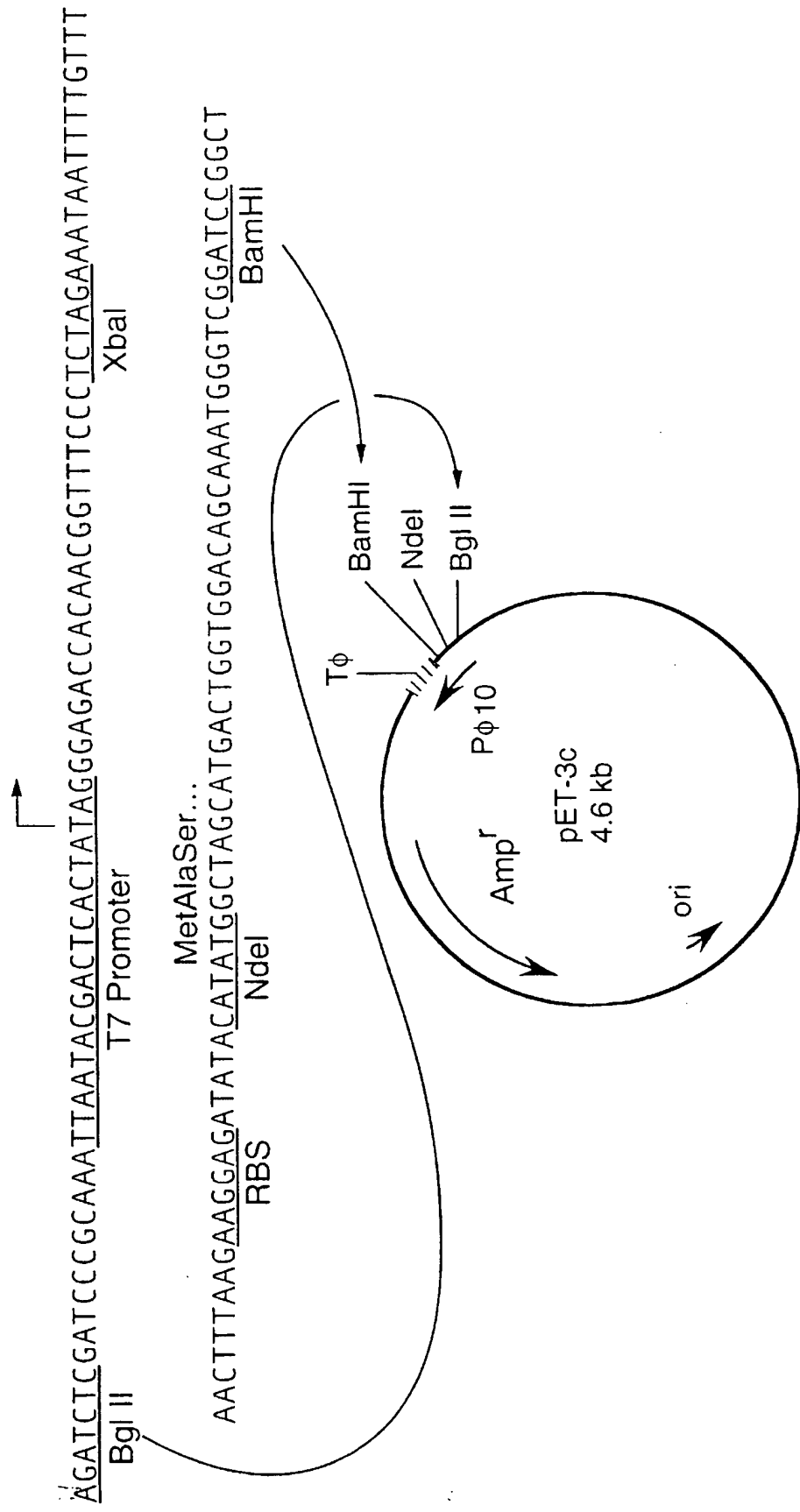


FIG. 12B



P_{φ10}: Bacteriophage T7 φ10 promoter RBS: Ribosome binding site
T_φ: T7 φ Terminator

FIG. 14

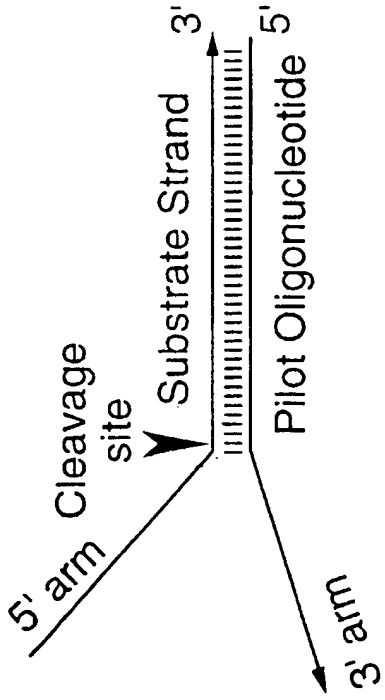


FIG. 15A

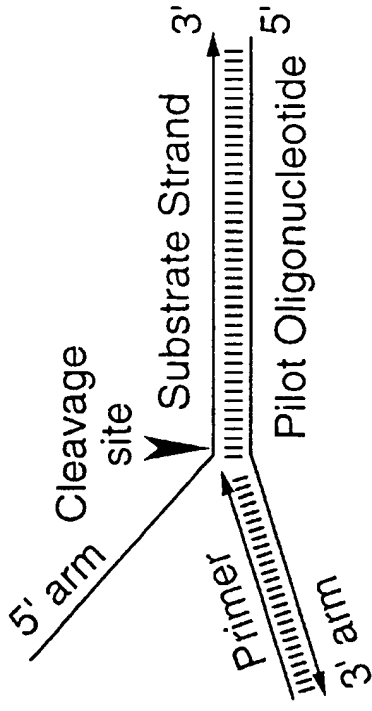


FIG. 15B

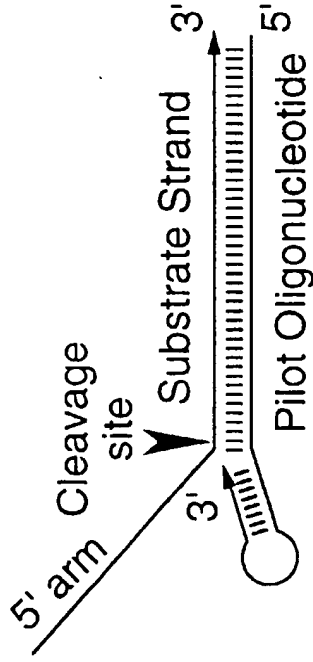


FIG. 15C

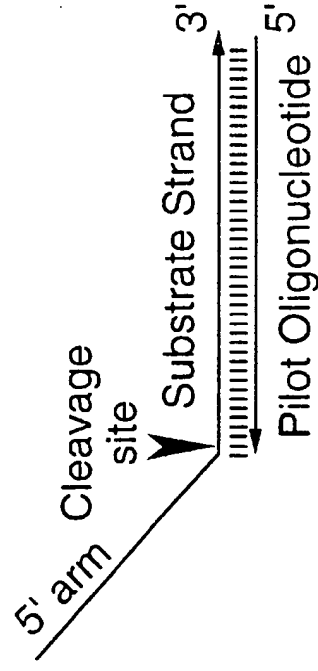


FIG. 15D

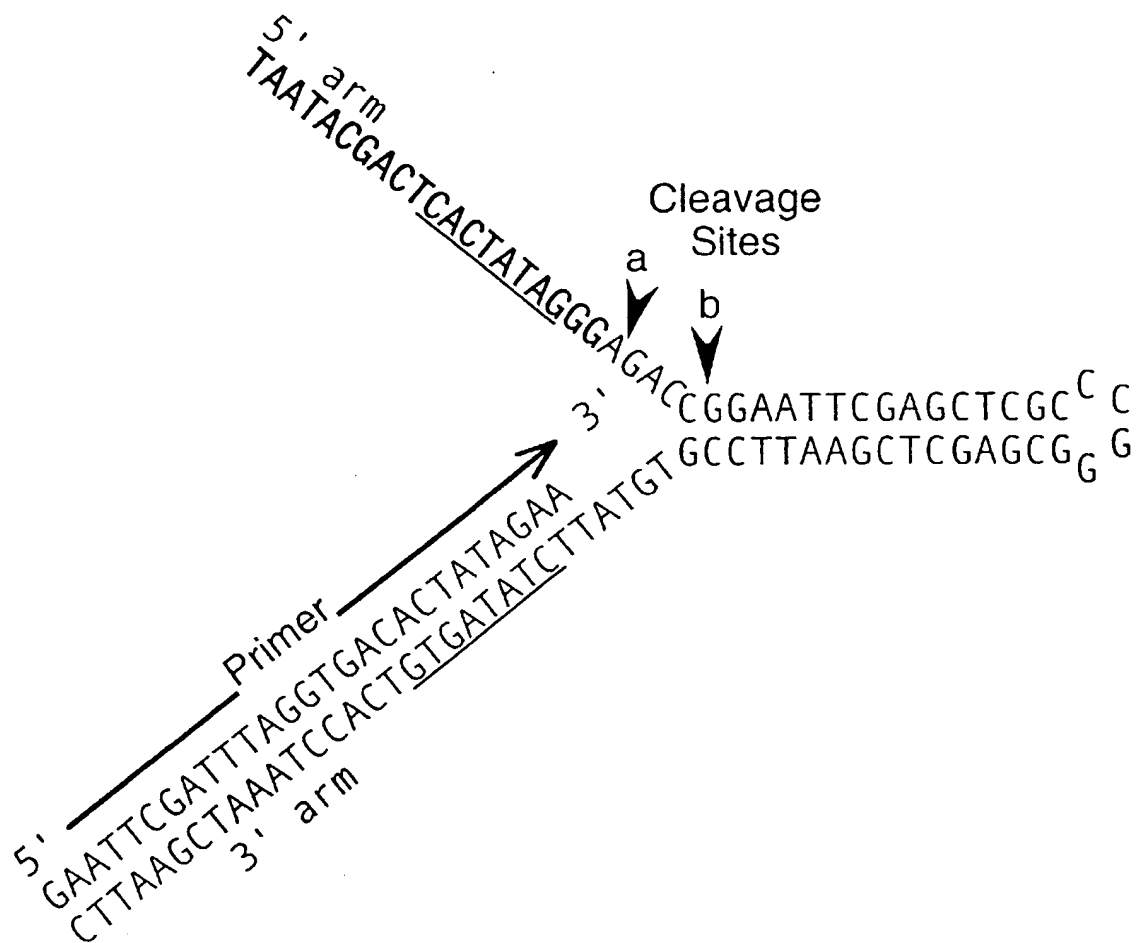
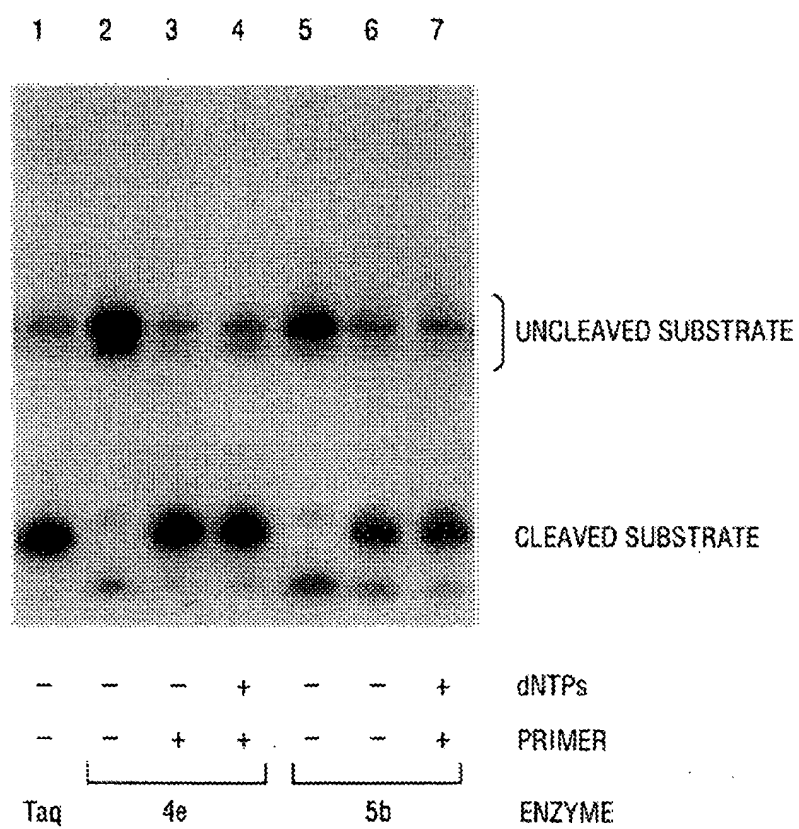


FIG. 15E

FIG. 16



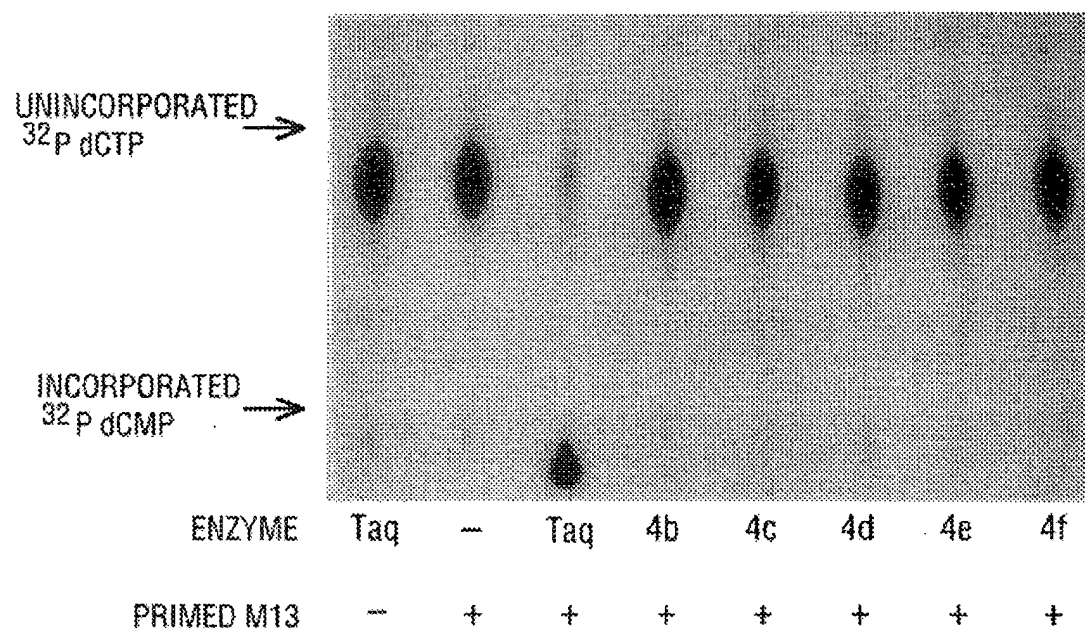


FIG. 17

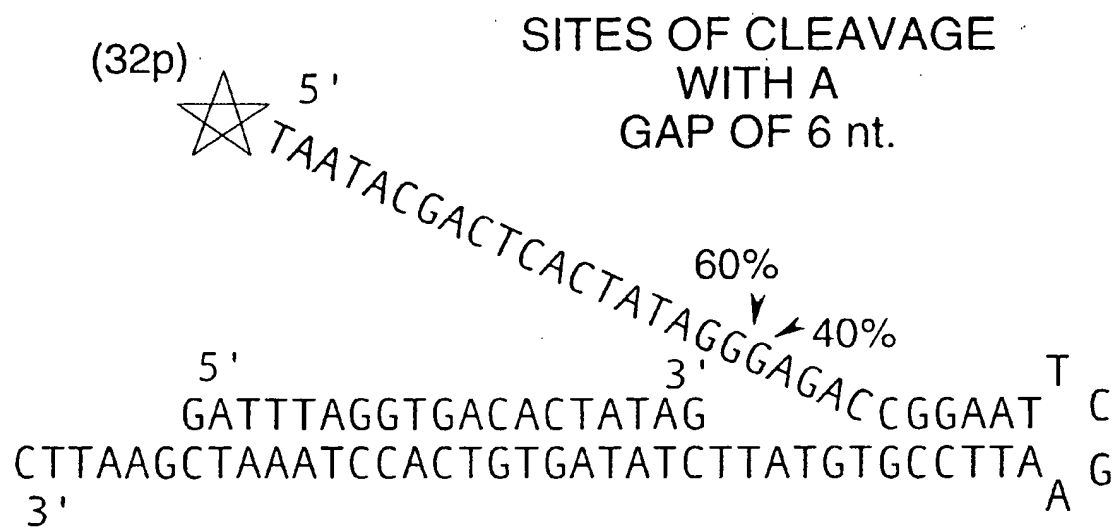


FIG. 18A

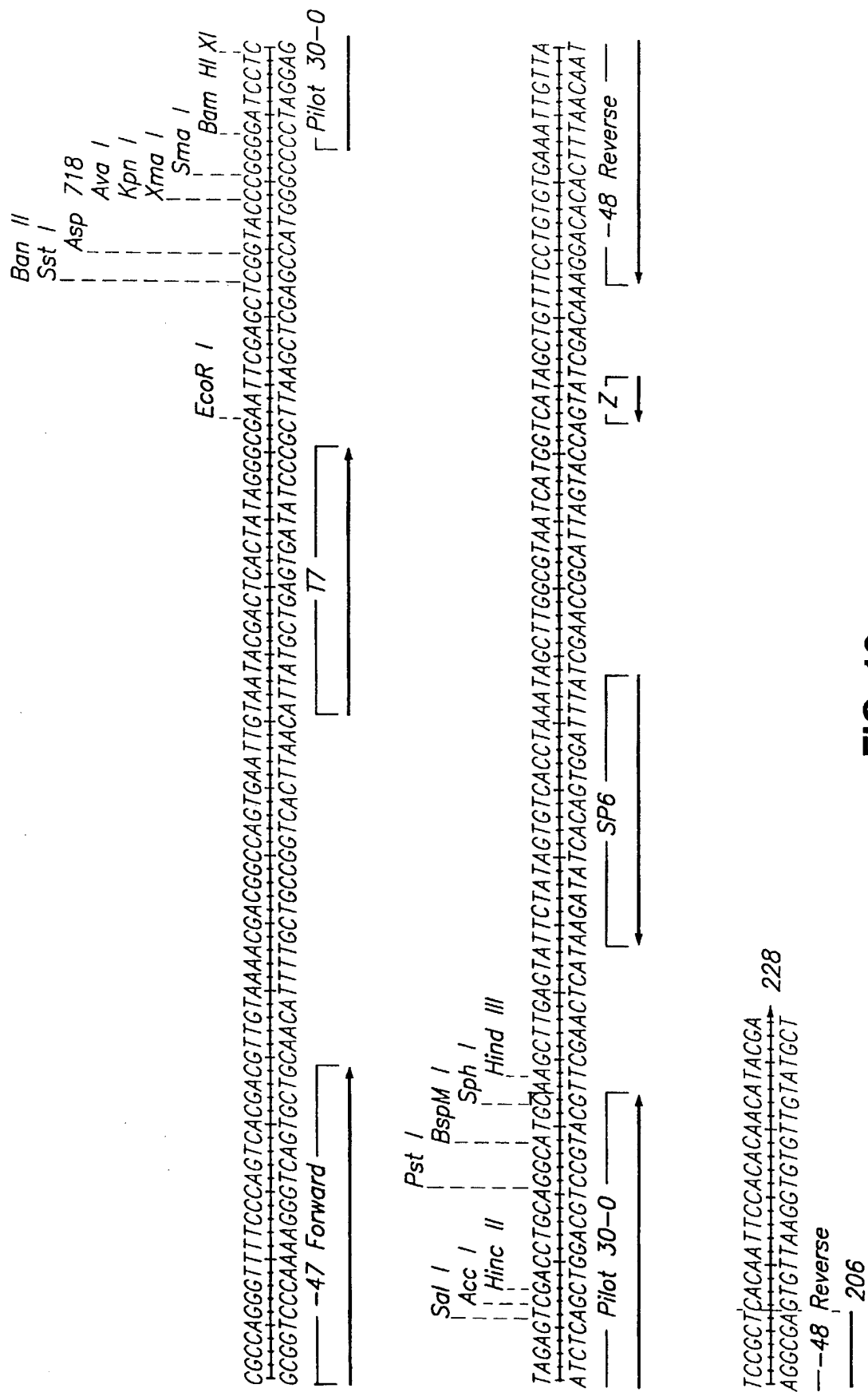


FIG. 19

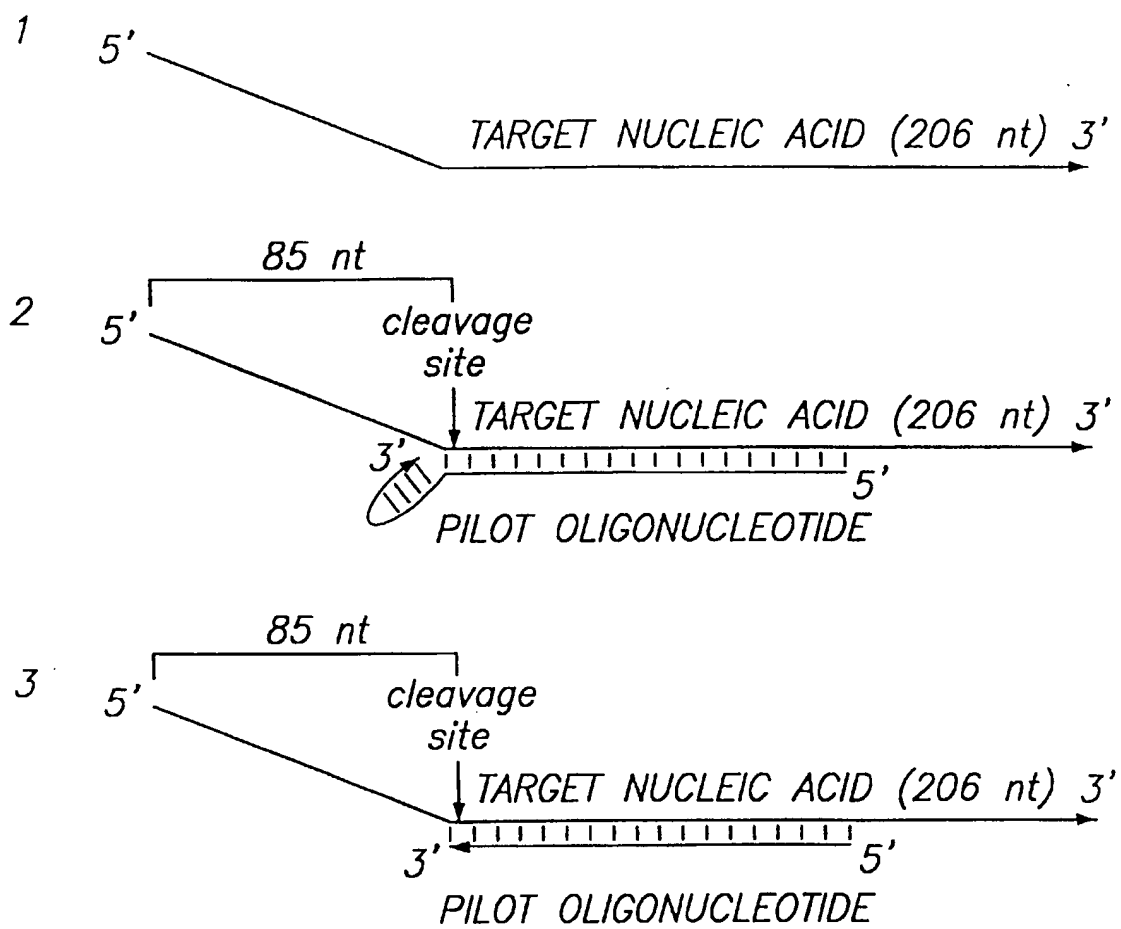


FIG. 20A

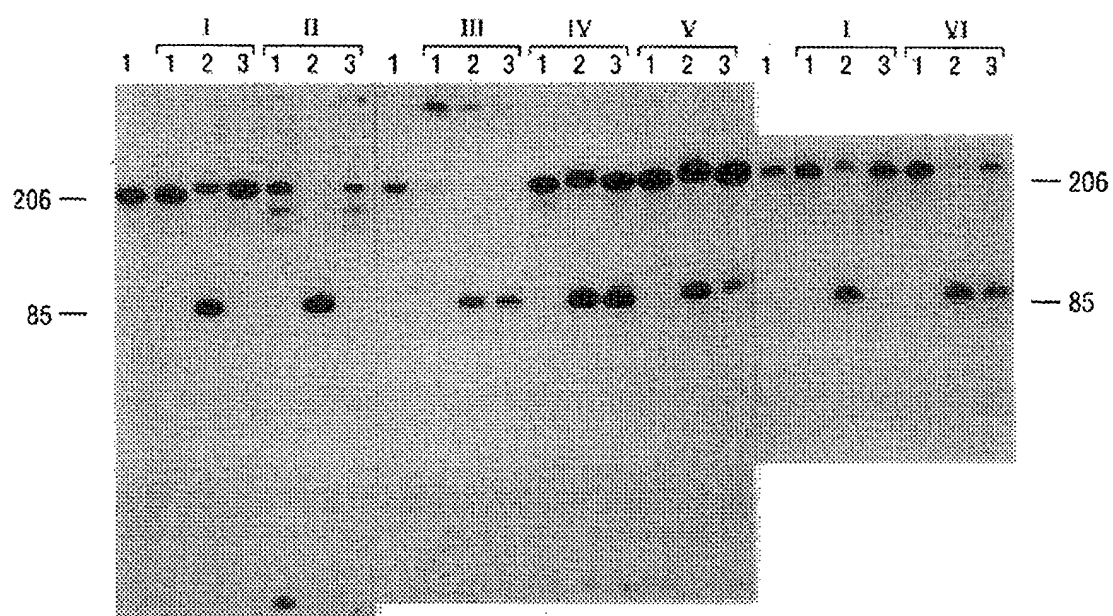


FIG. 20B

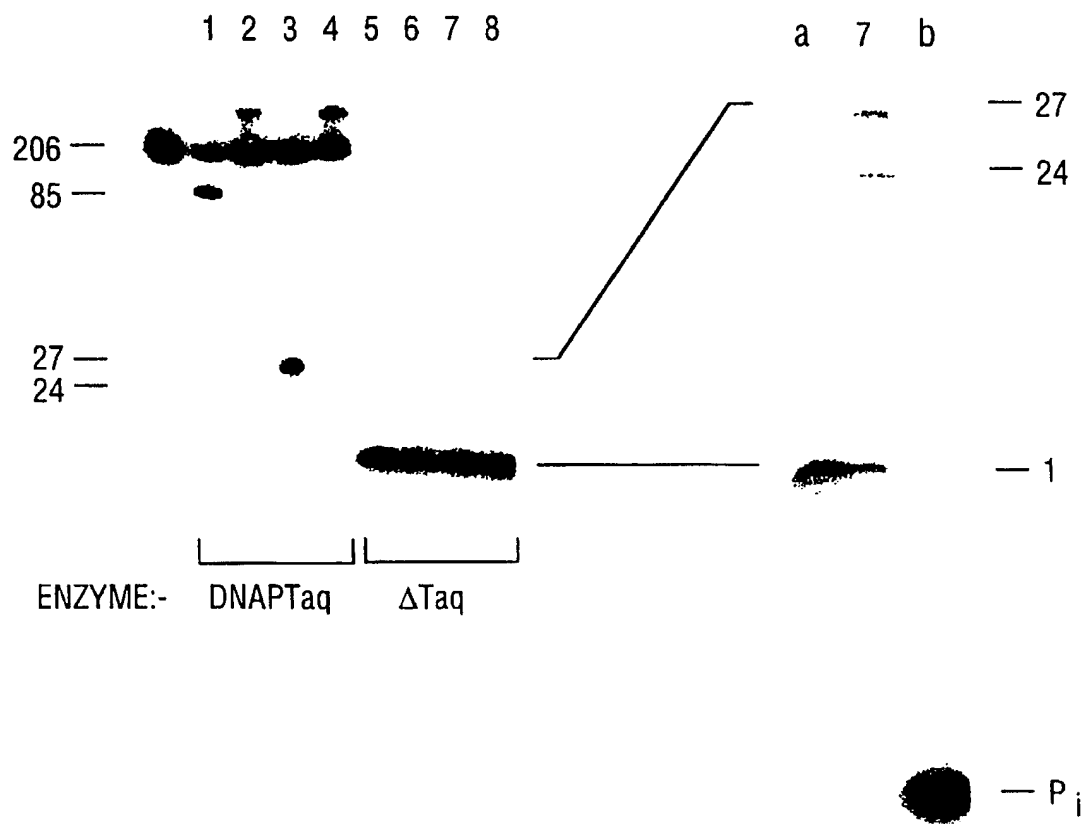


FIG. 21A

FIG. 21B

FIG. 22A

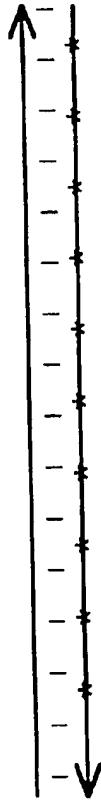
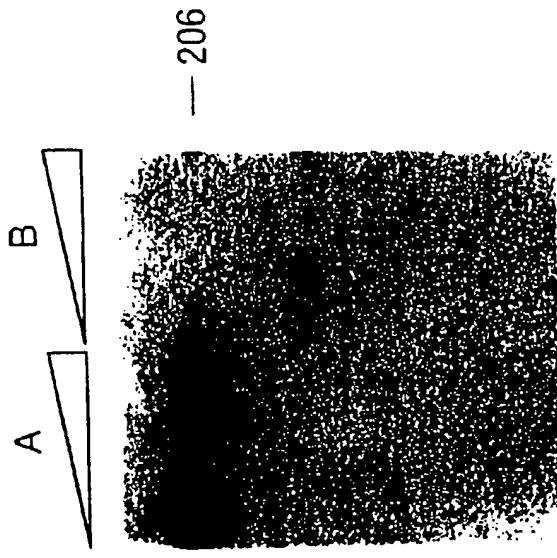


FIG. 22B

* = 32p



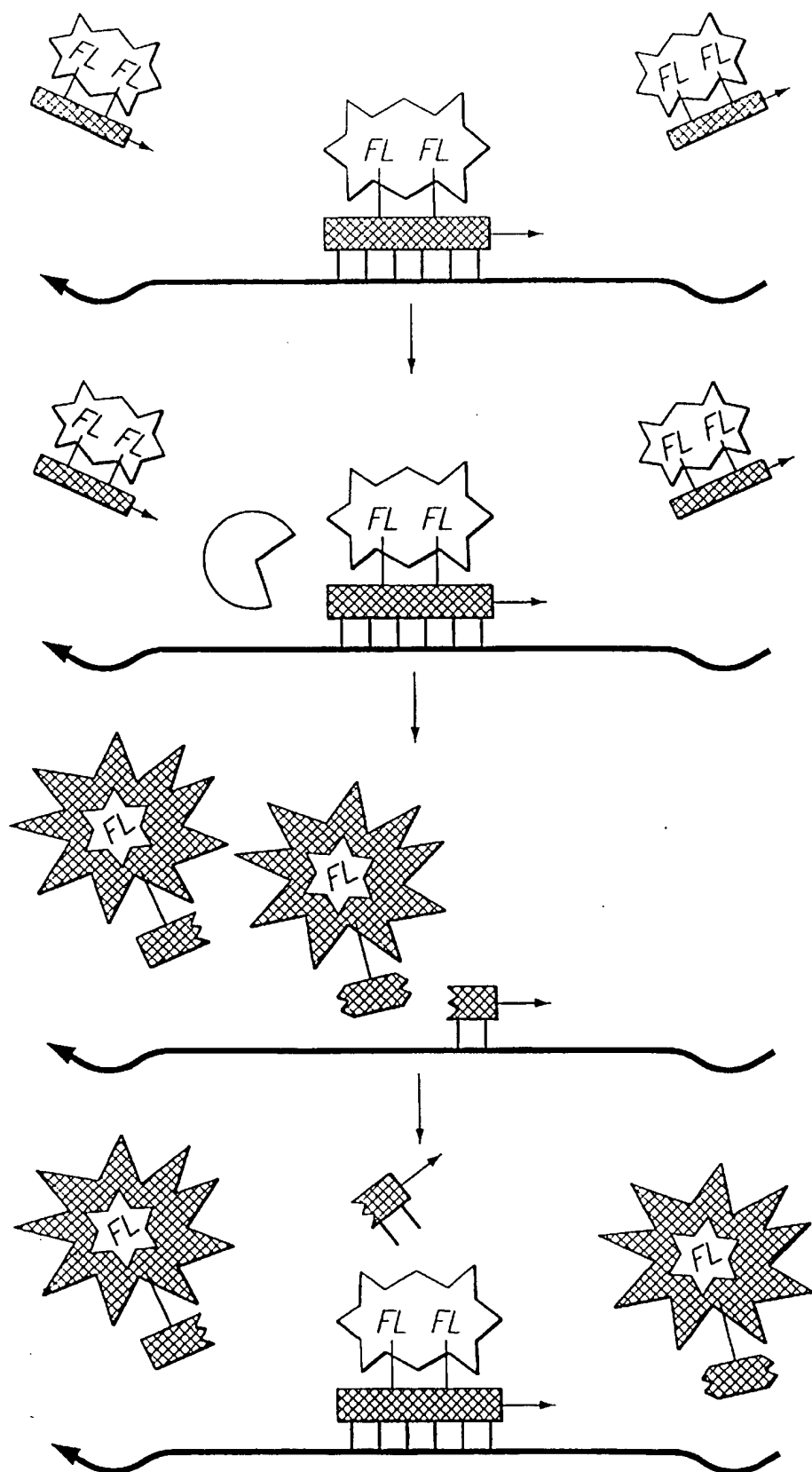


FIG. 23

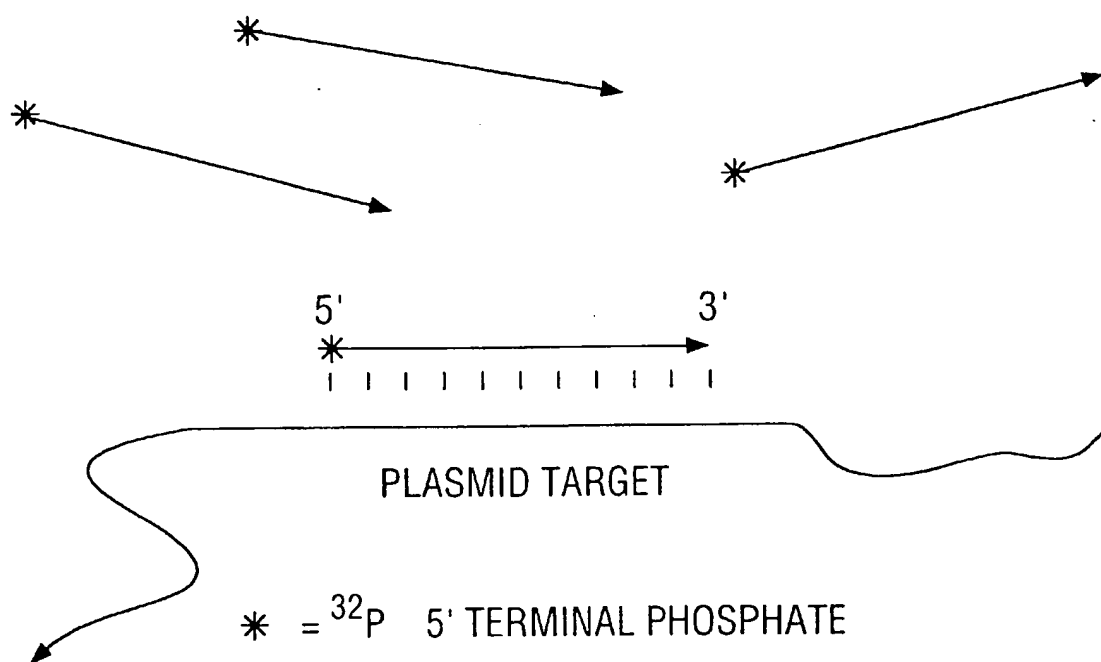


FIG. 24A

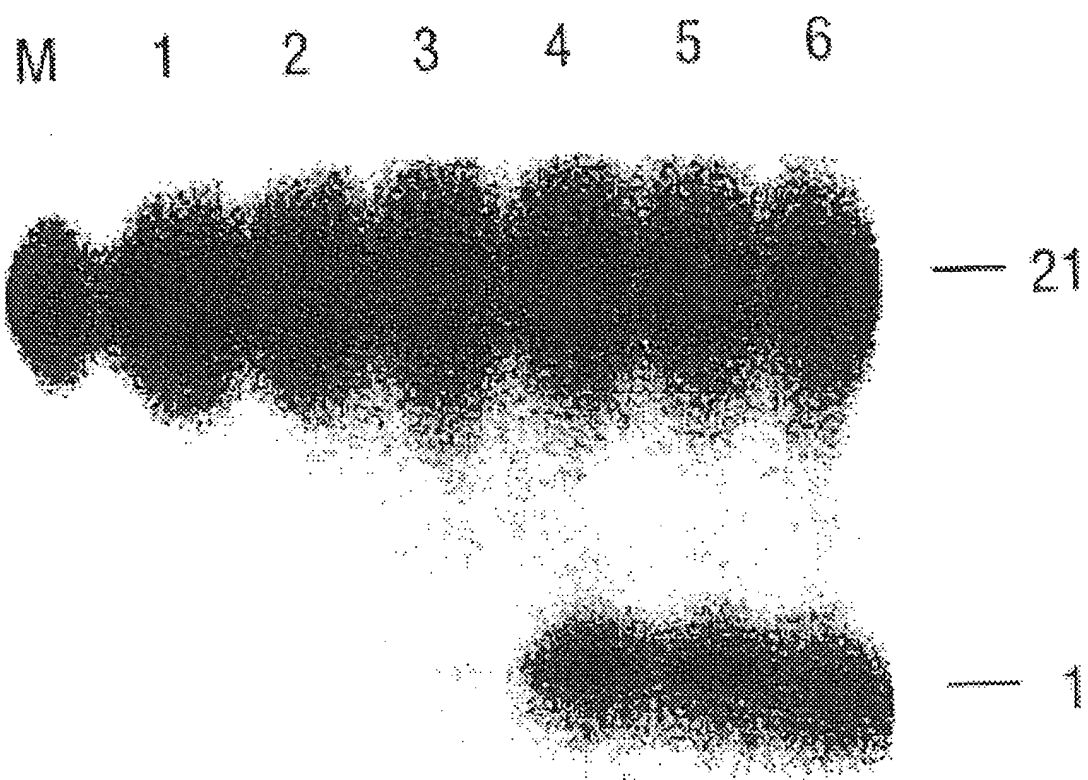


FIG. 24B

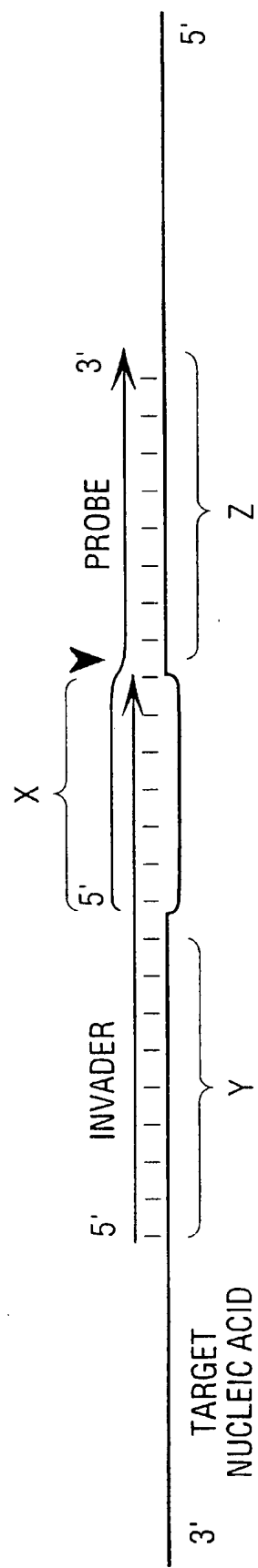


FIG. 25

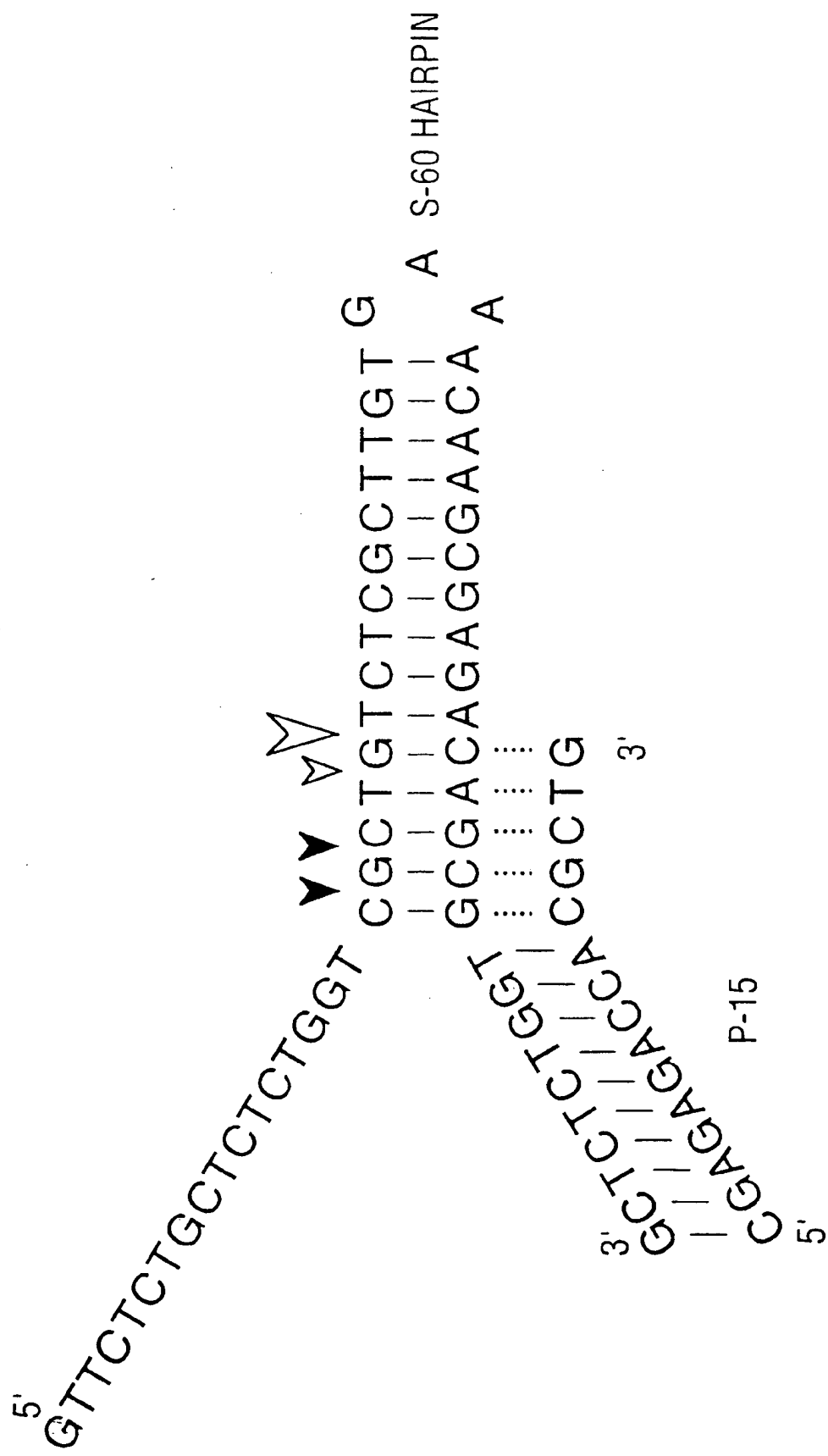


FIG. 26

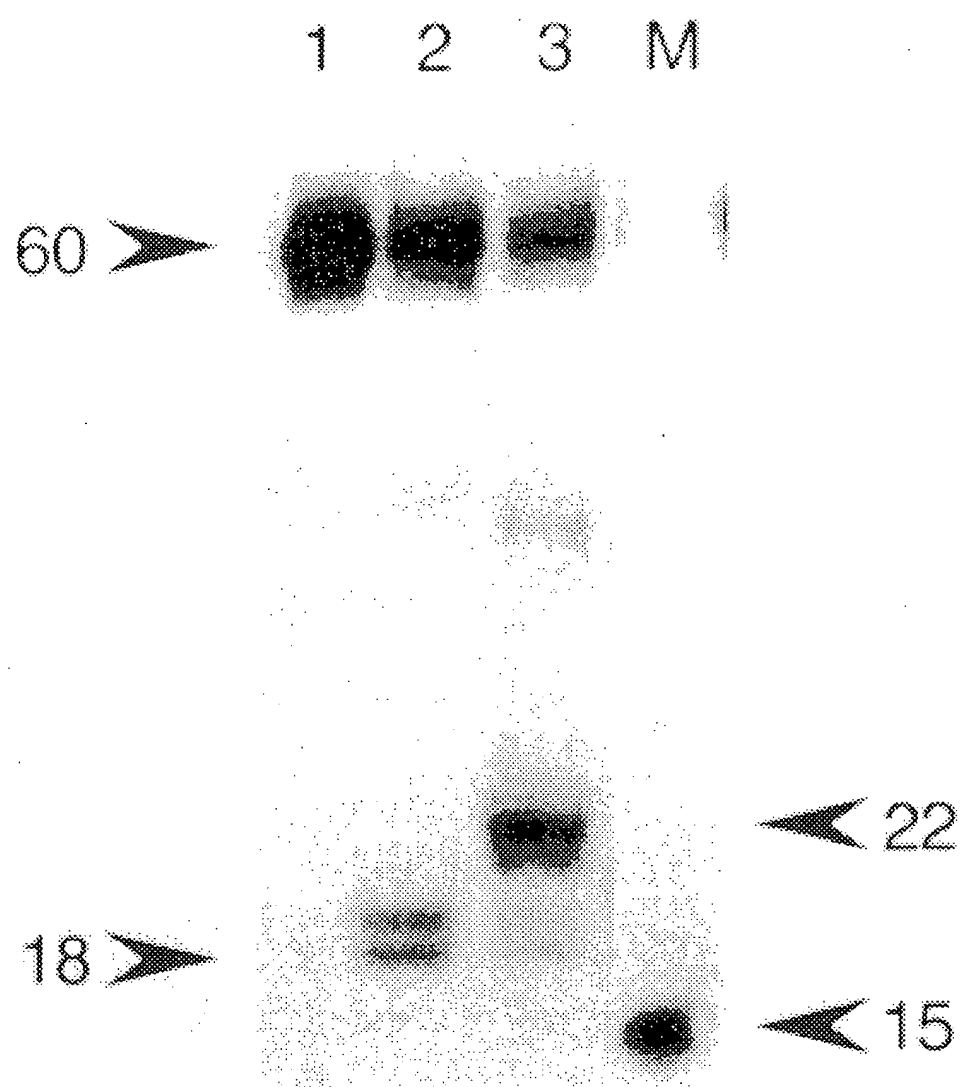


FIG. 27

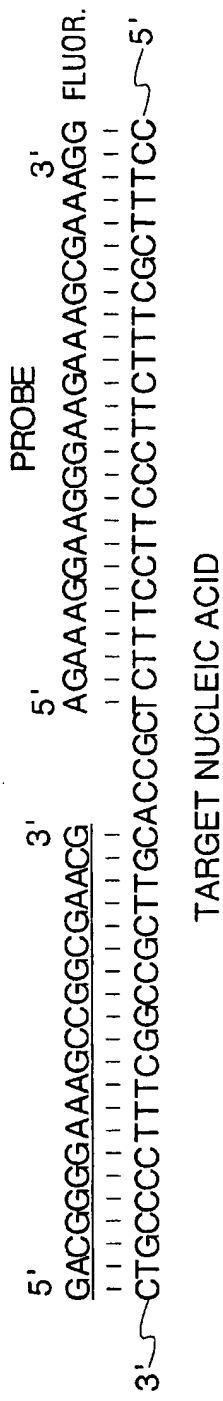


FIG. 28A

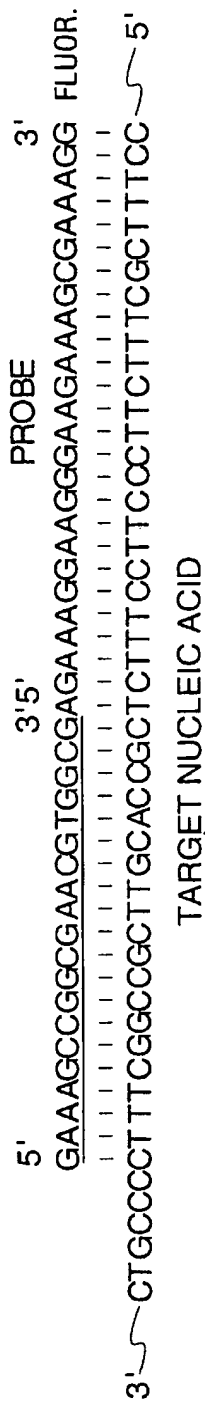


FIG. 28B

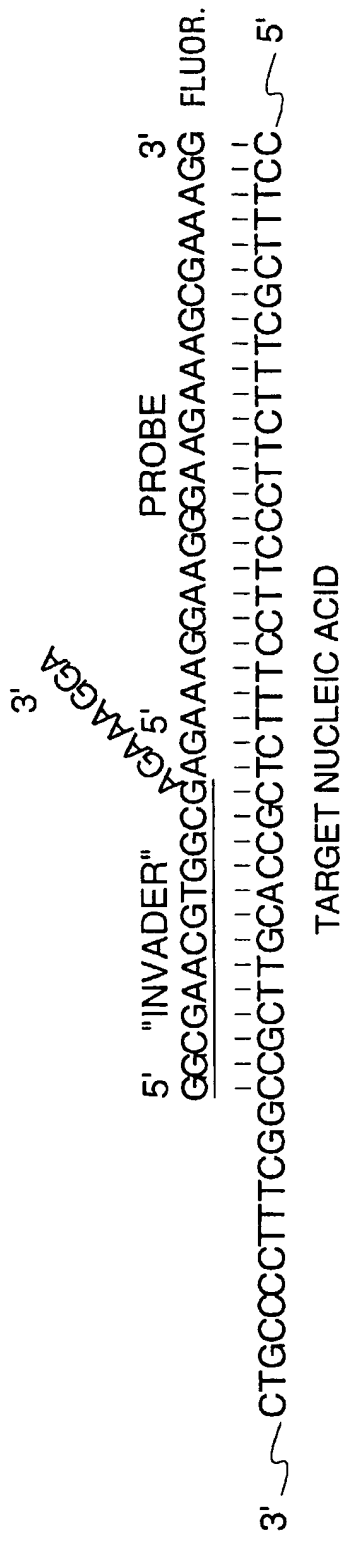


FIG. 28C

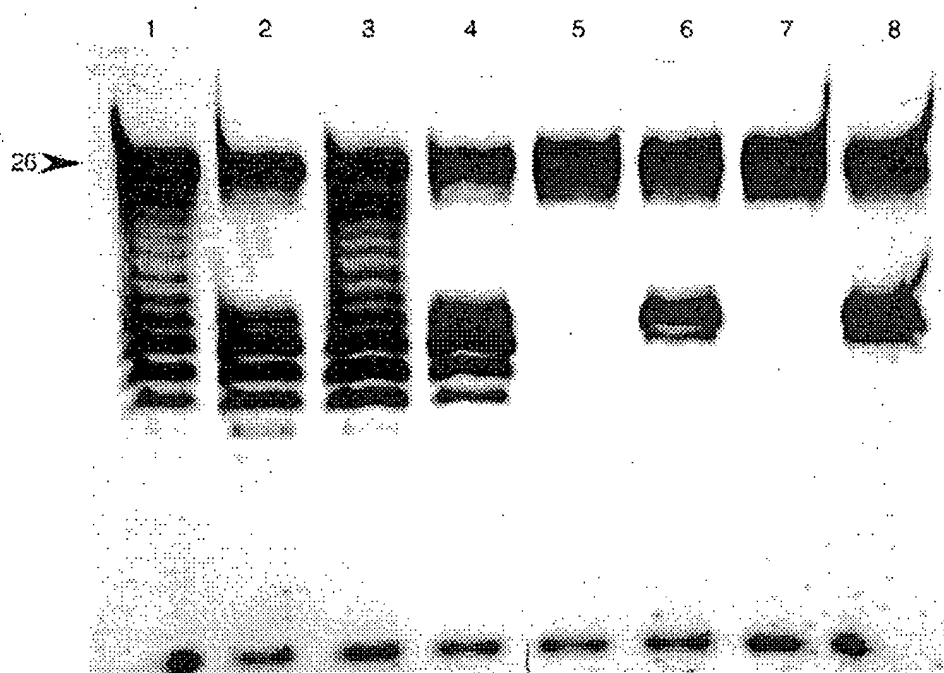


FIG. 29

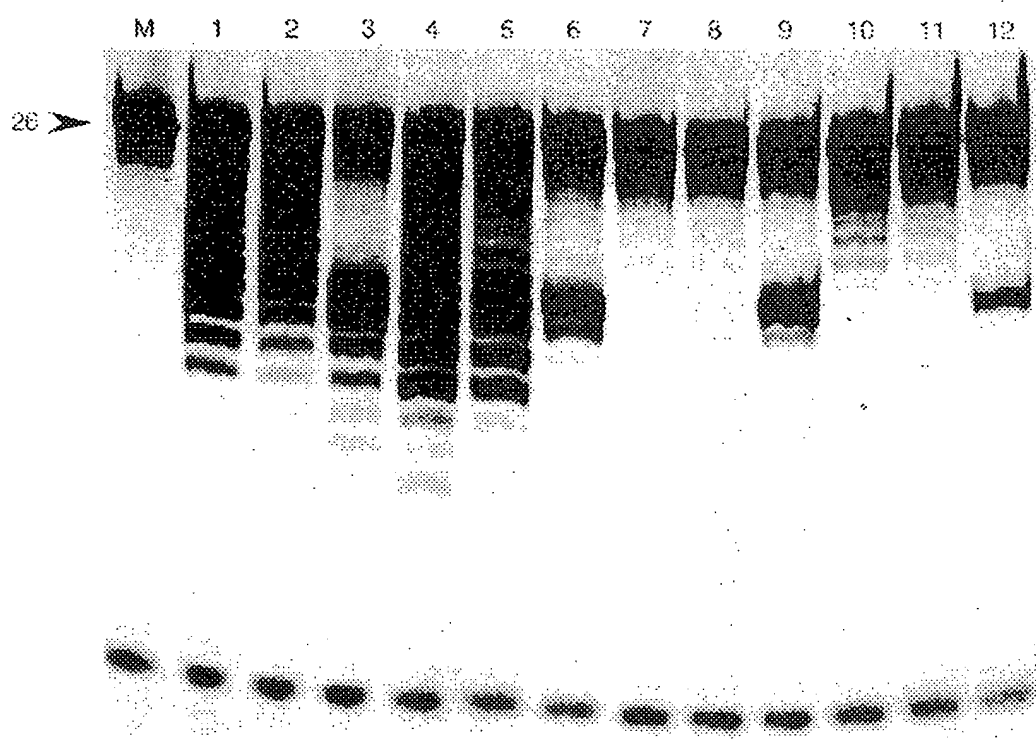


FIG. 30

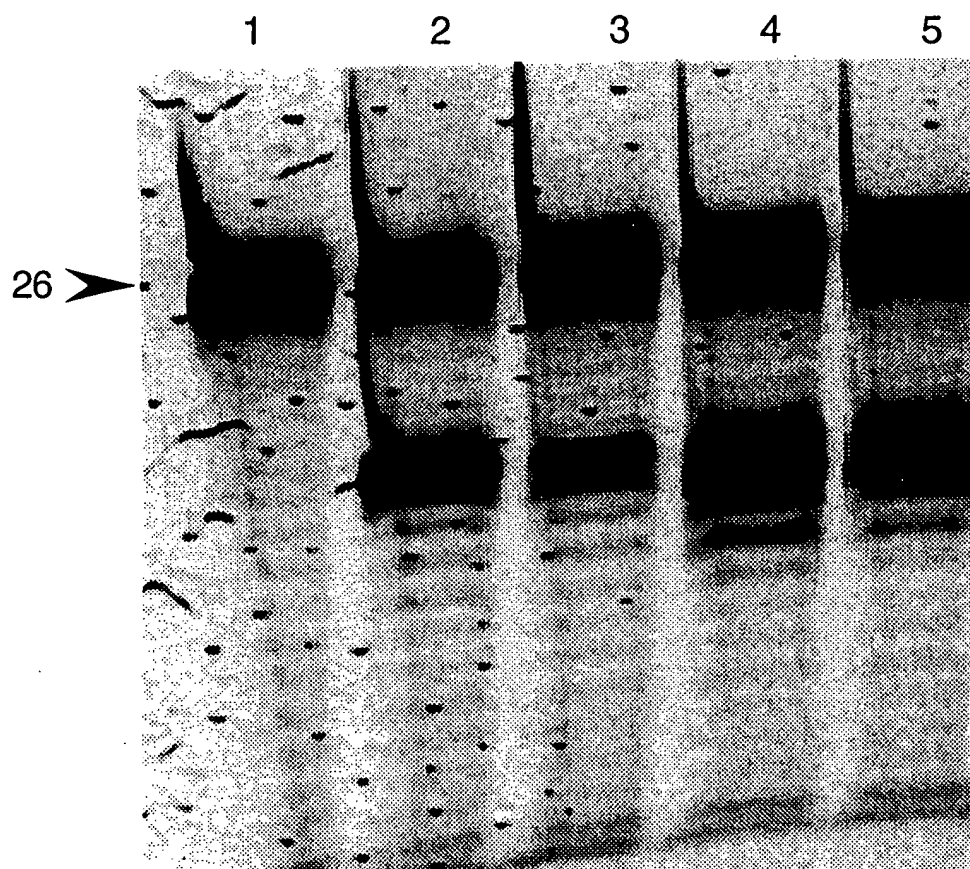


FIG. 31

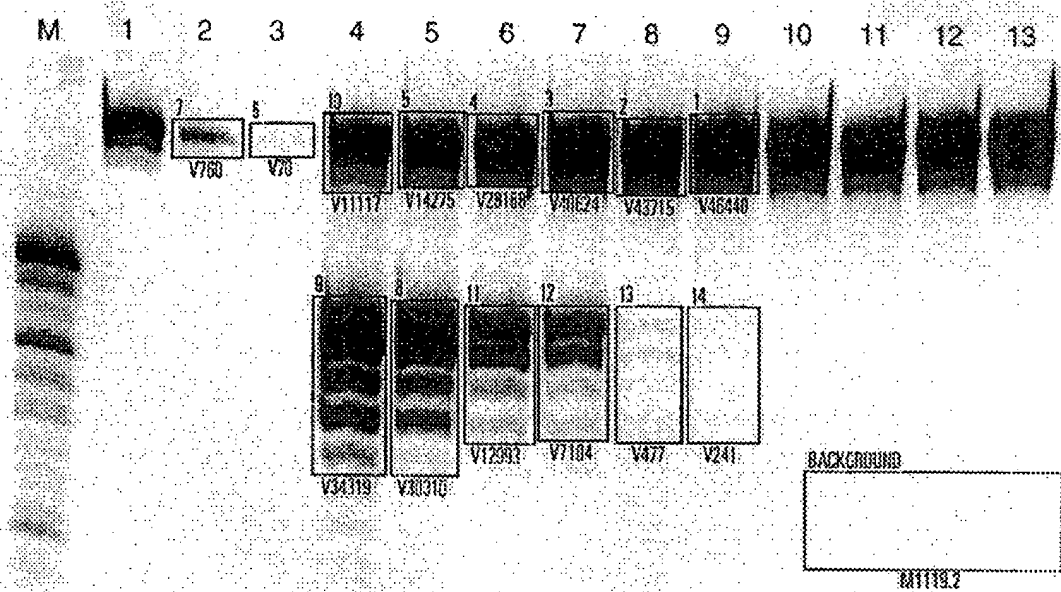


FIG. 32

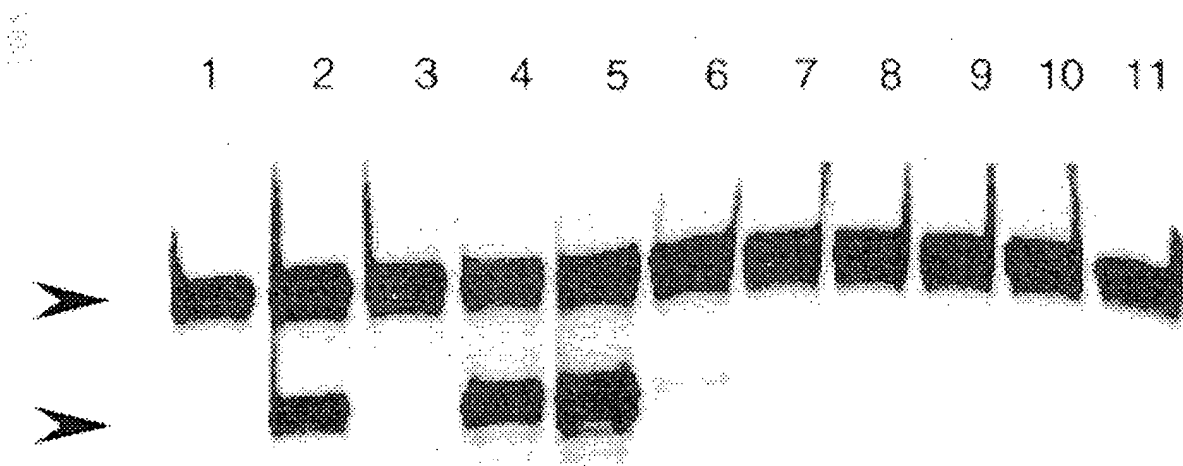


FIG. 33

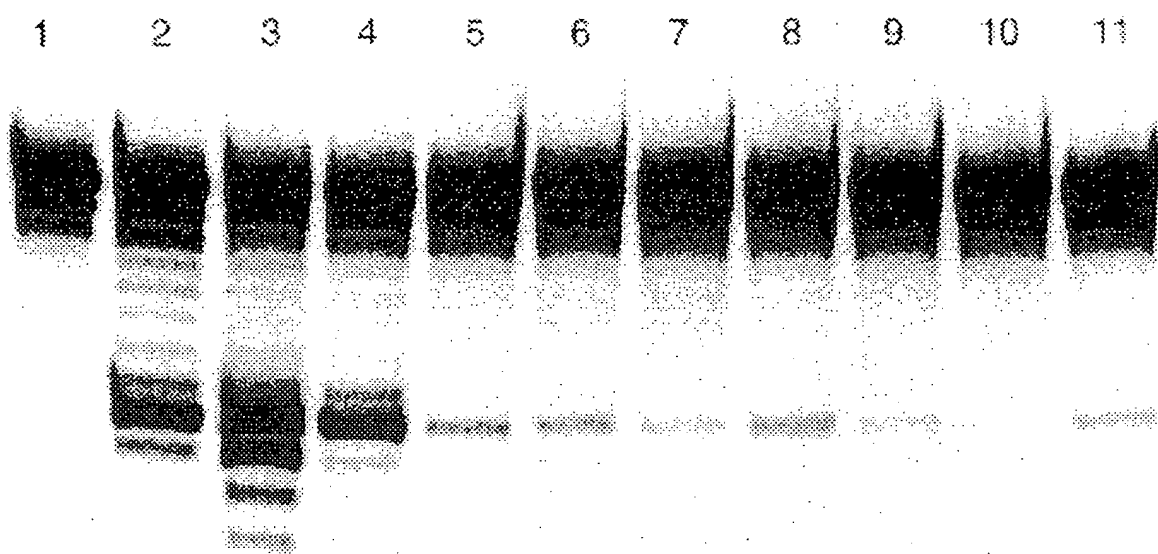


FIG. 34

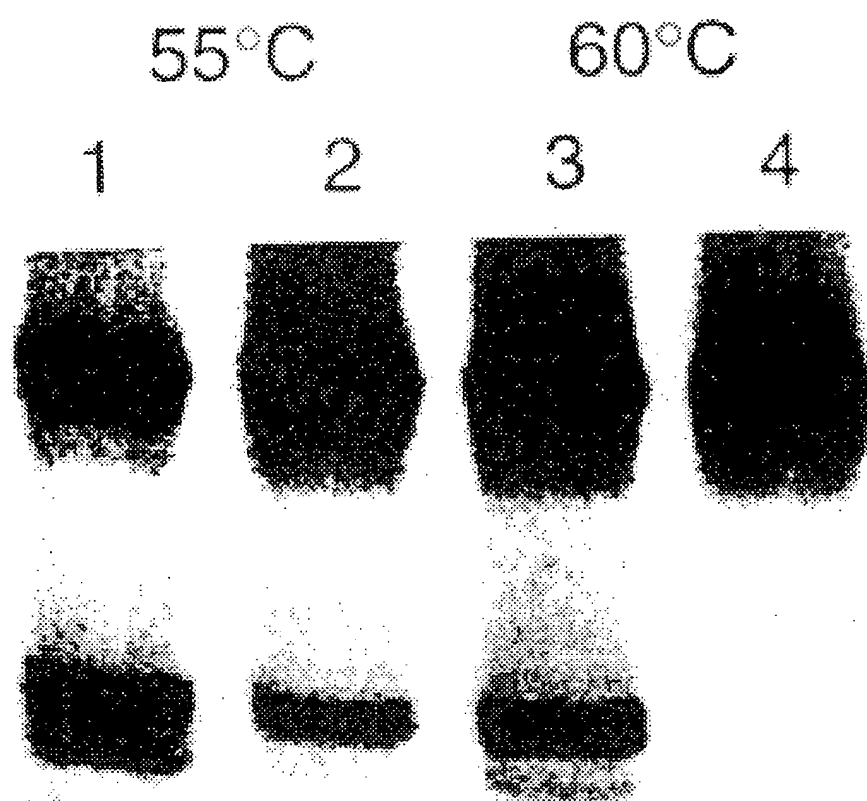


FIG. 35

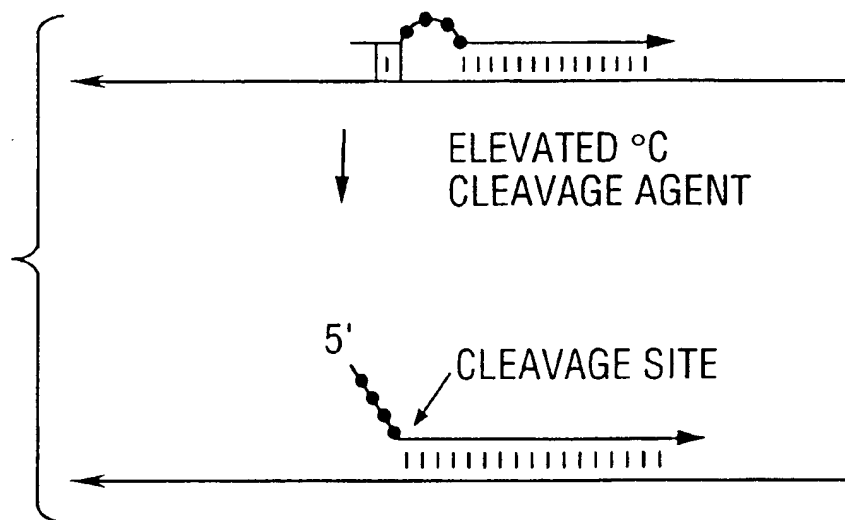


FIG. 36A

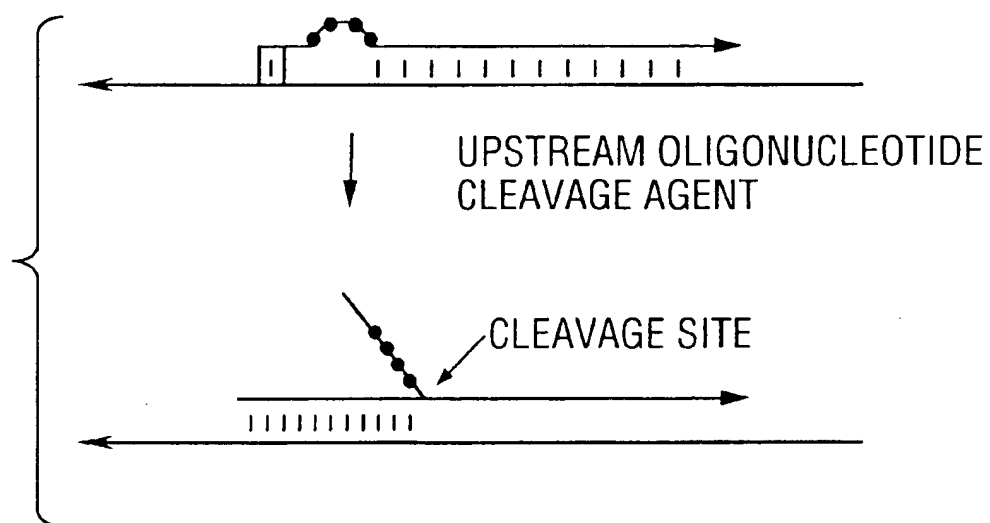


FIG. 36B

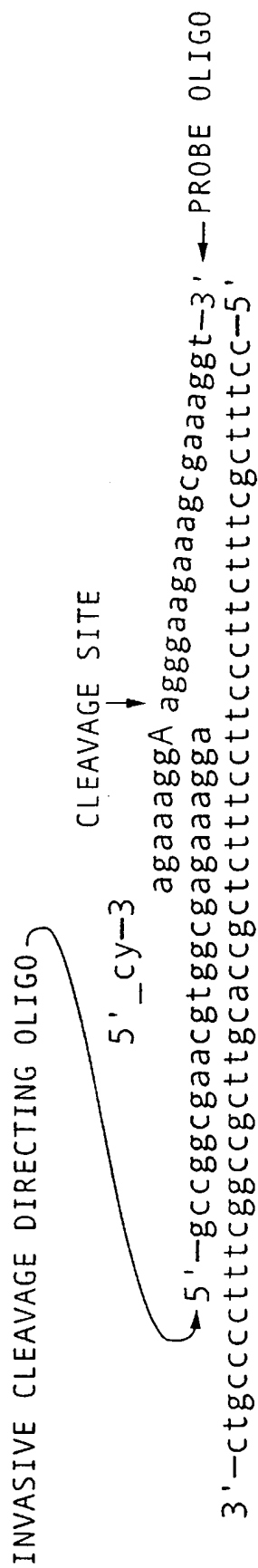


FIG. 37

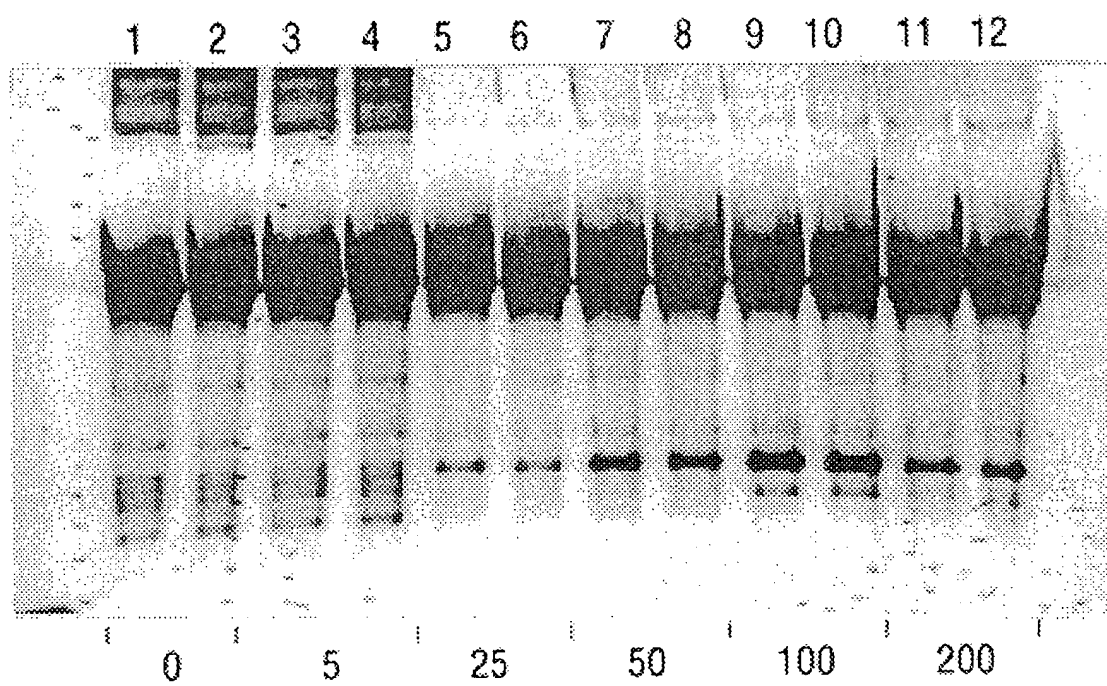


FIG. 38

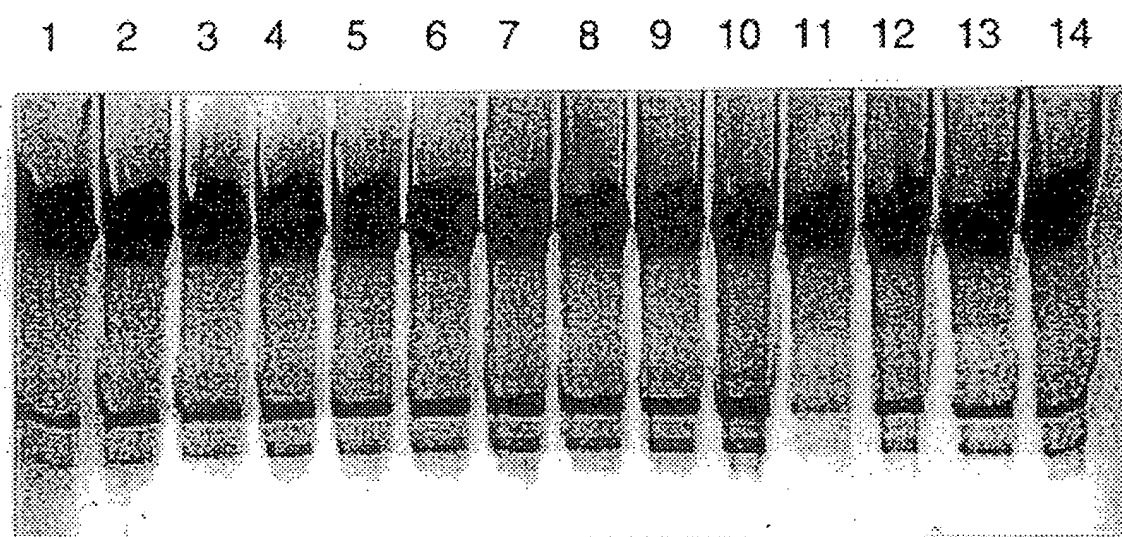


FIG. 39

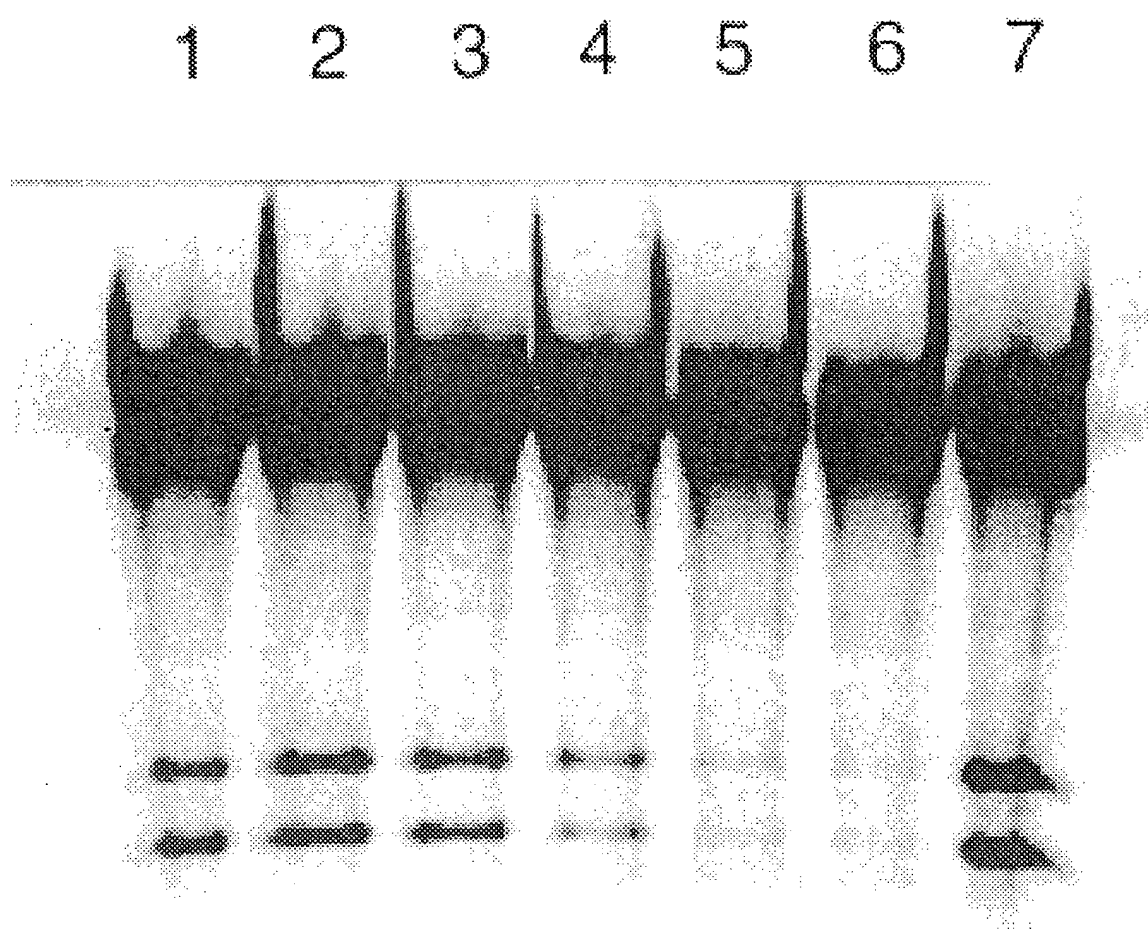


FIG. 40

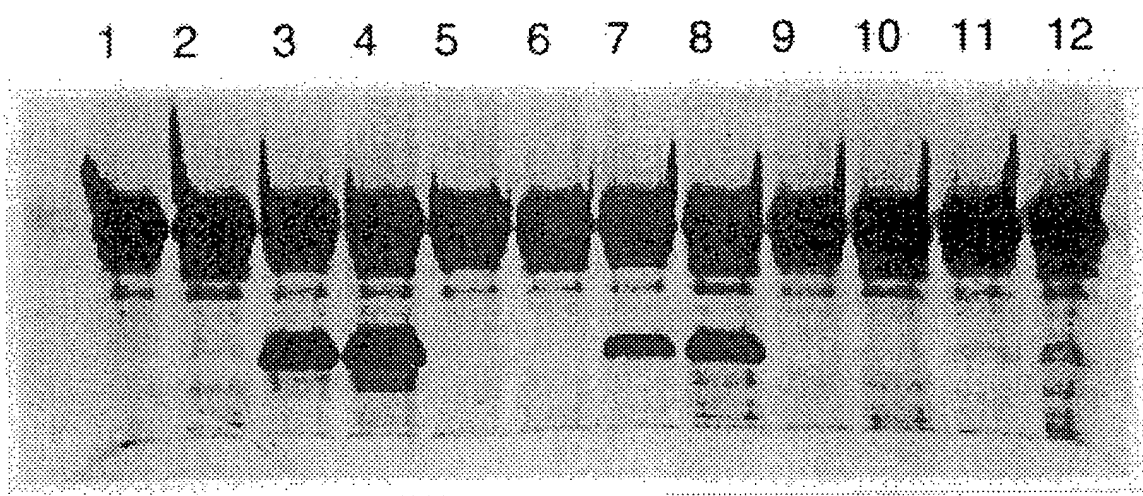
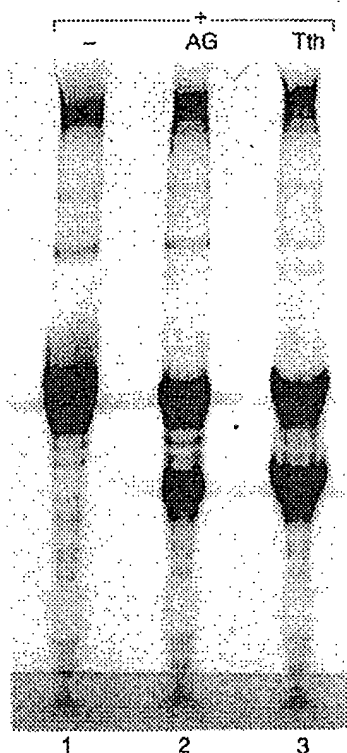
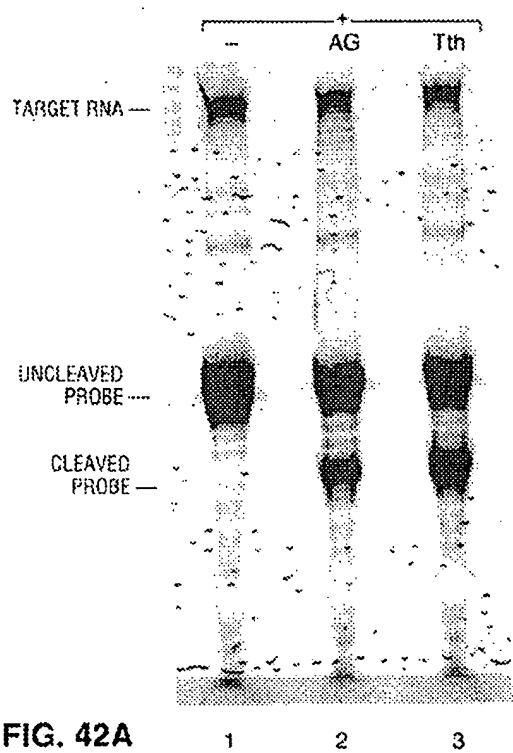


FIG. 41



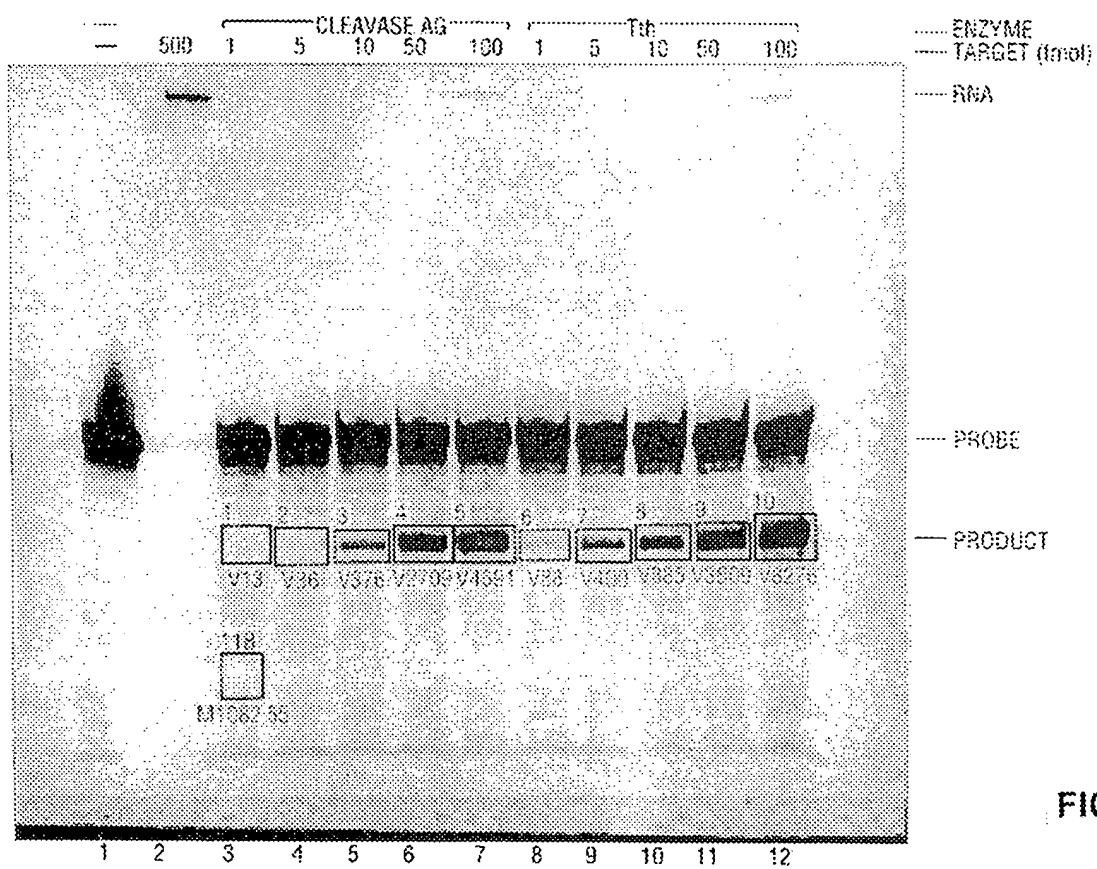


FIG. 43

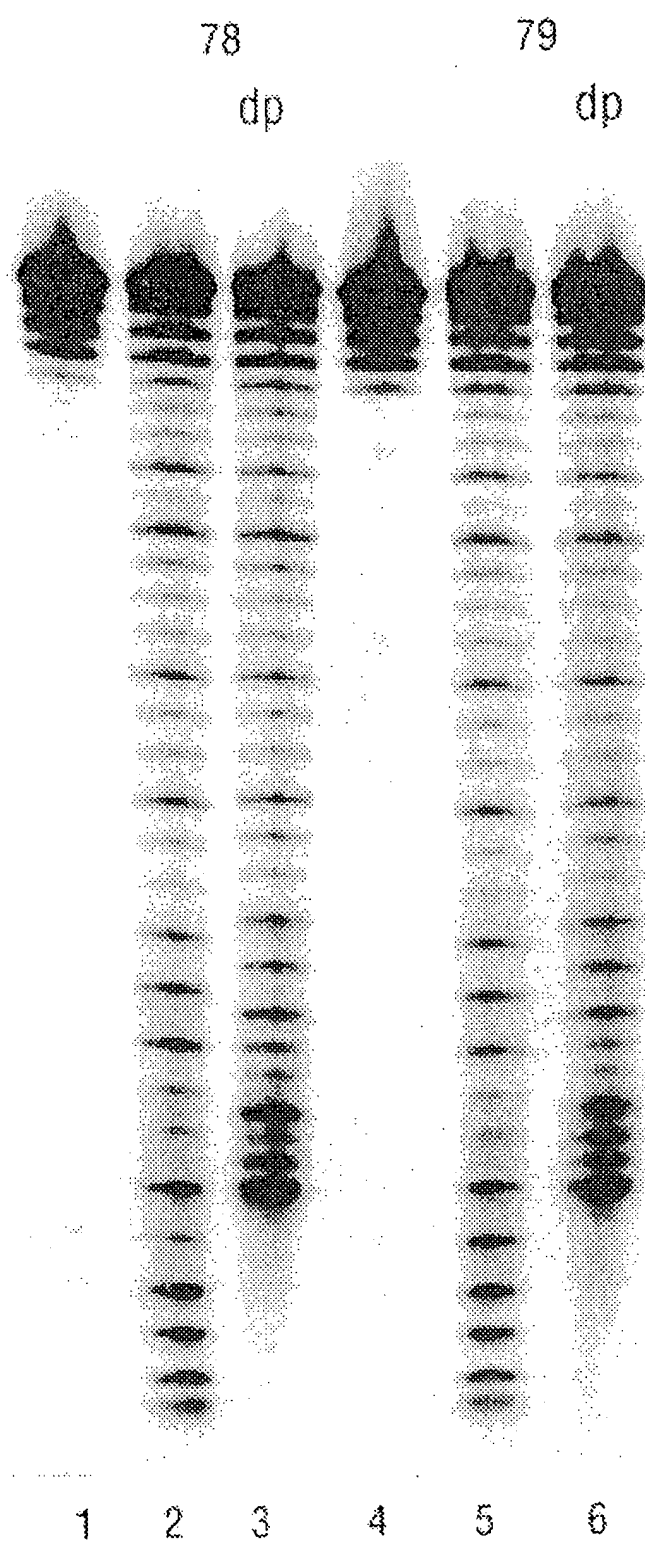


FIG. 44

70 (C10 amino T's)
74 (C6 amino T's)

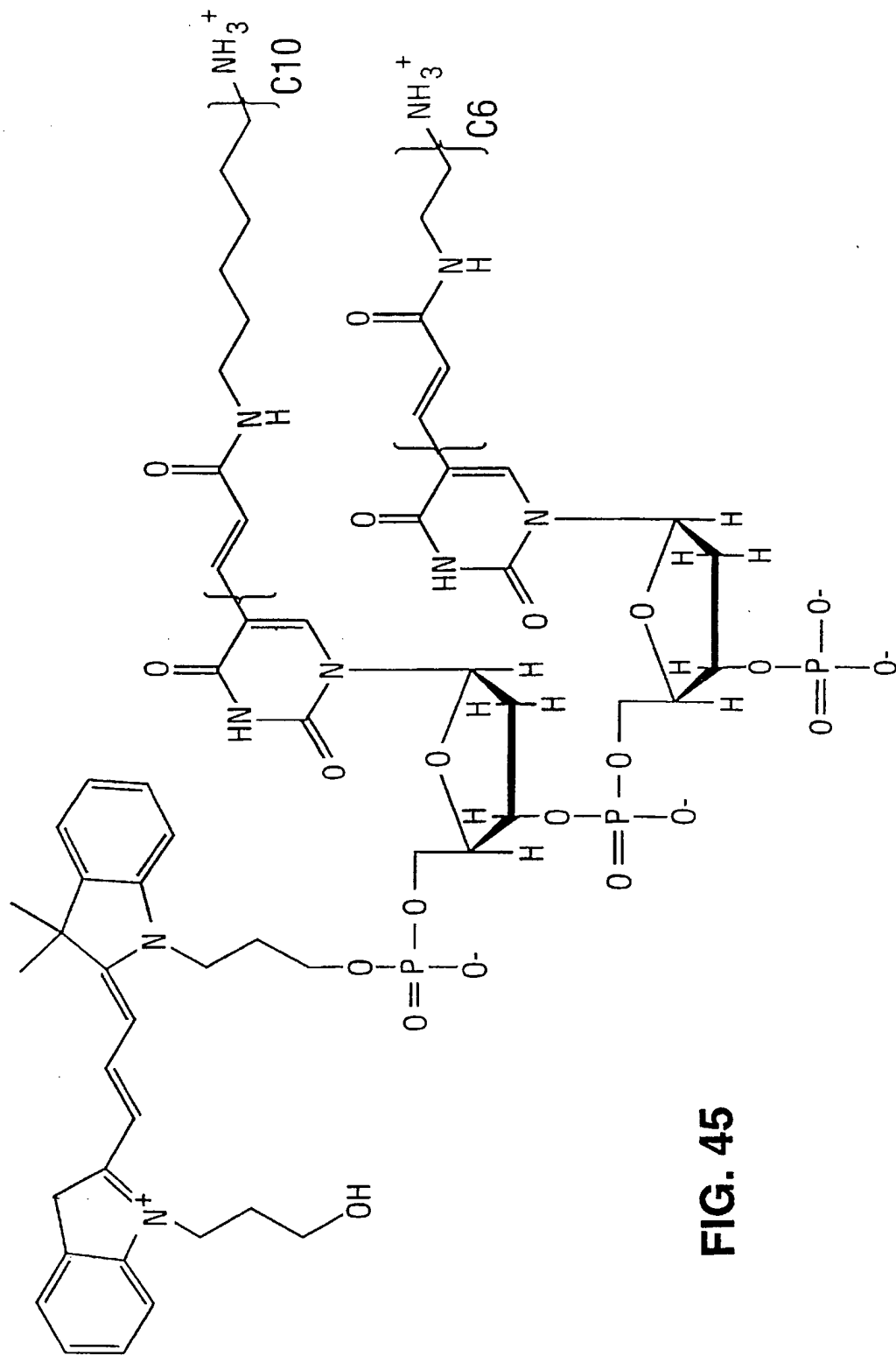


FIG. 45

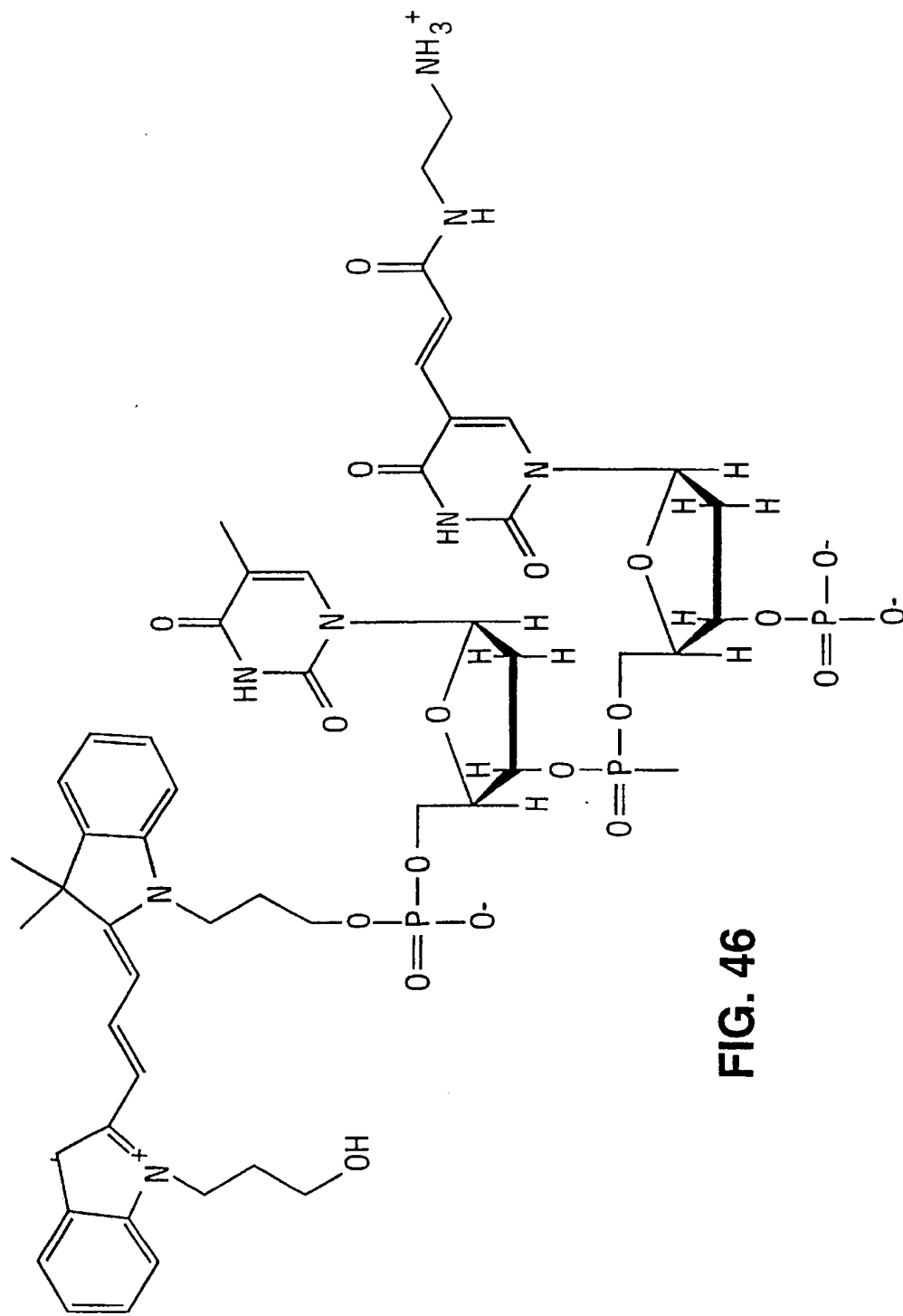


FIG. 46

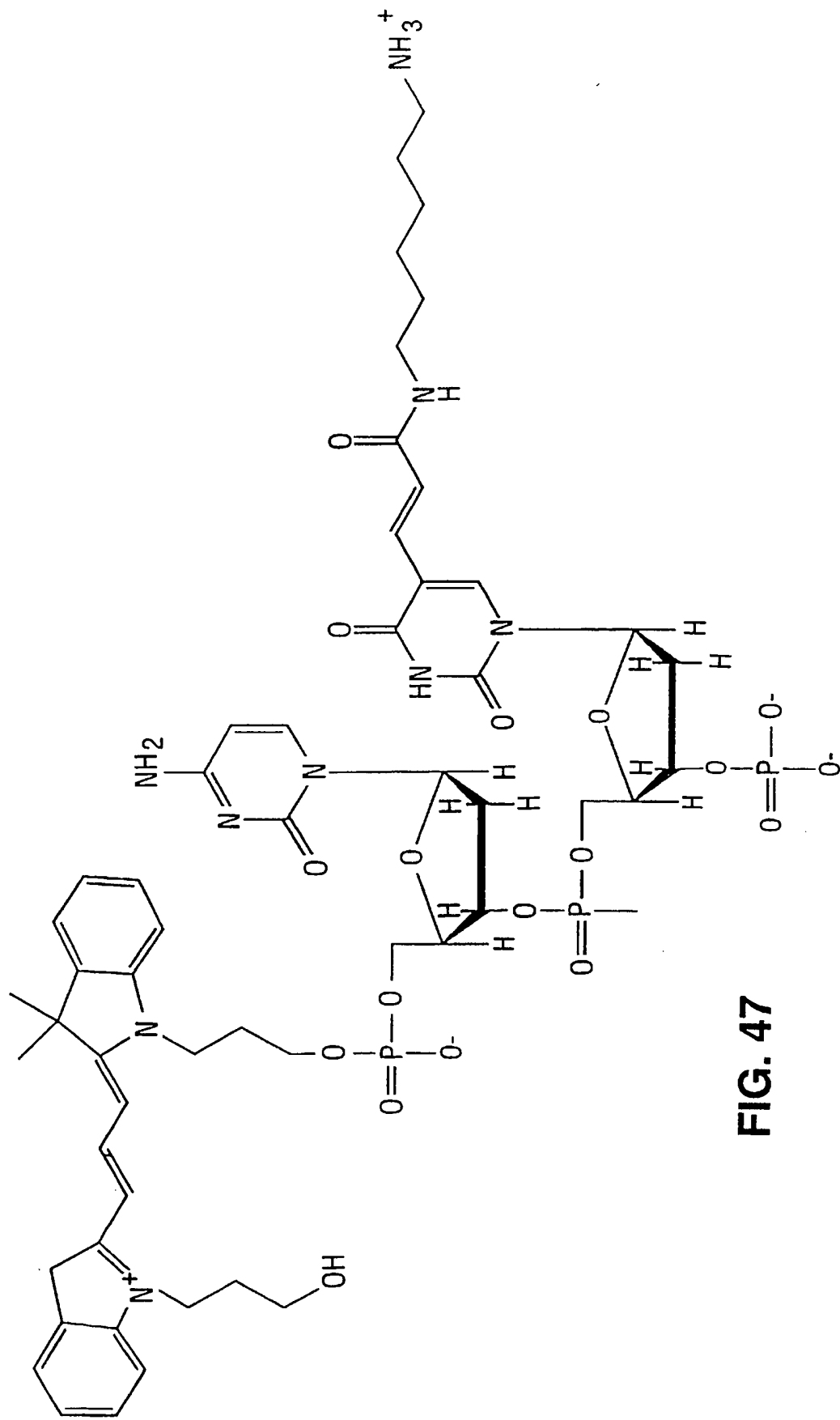


FIG. 47

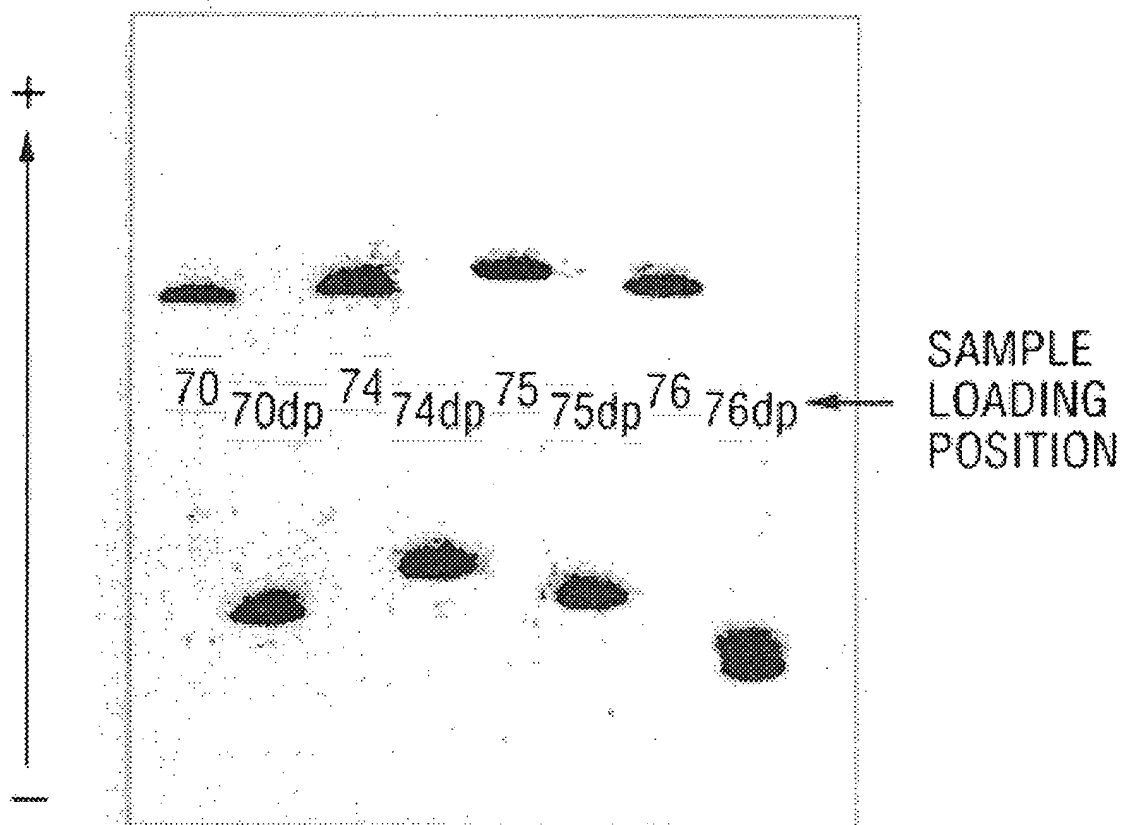


FIG. 48

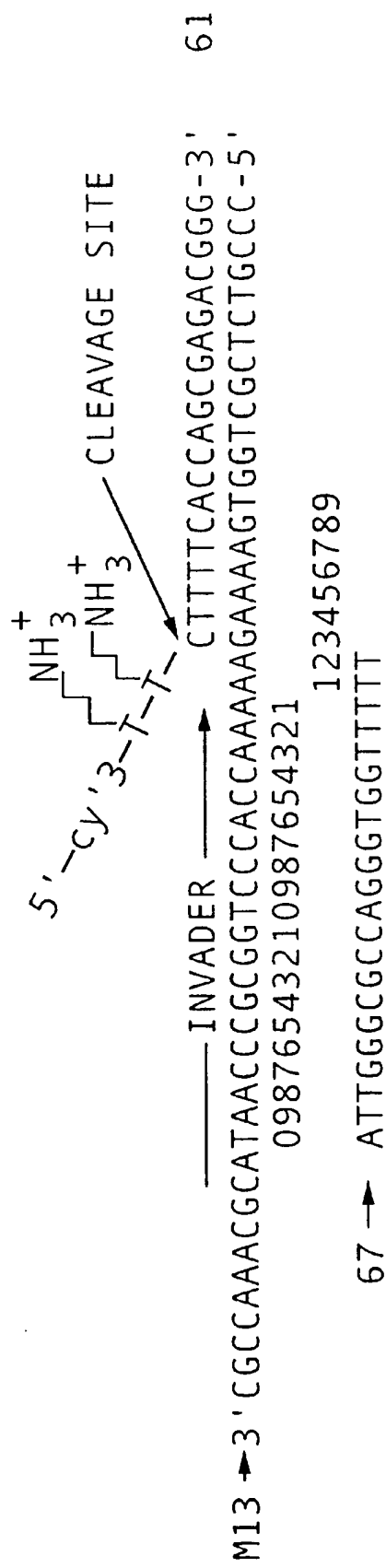


FIG. 49A

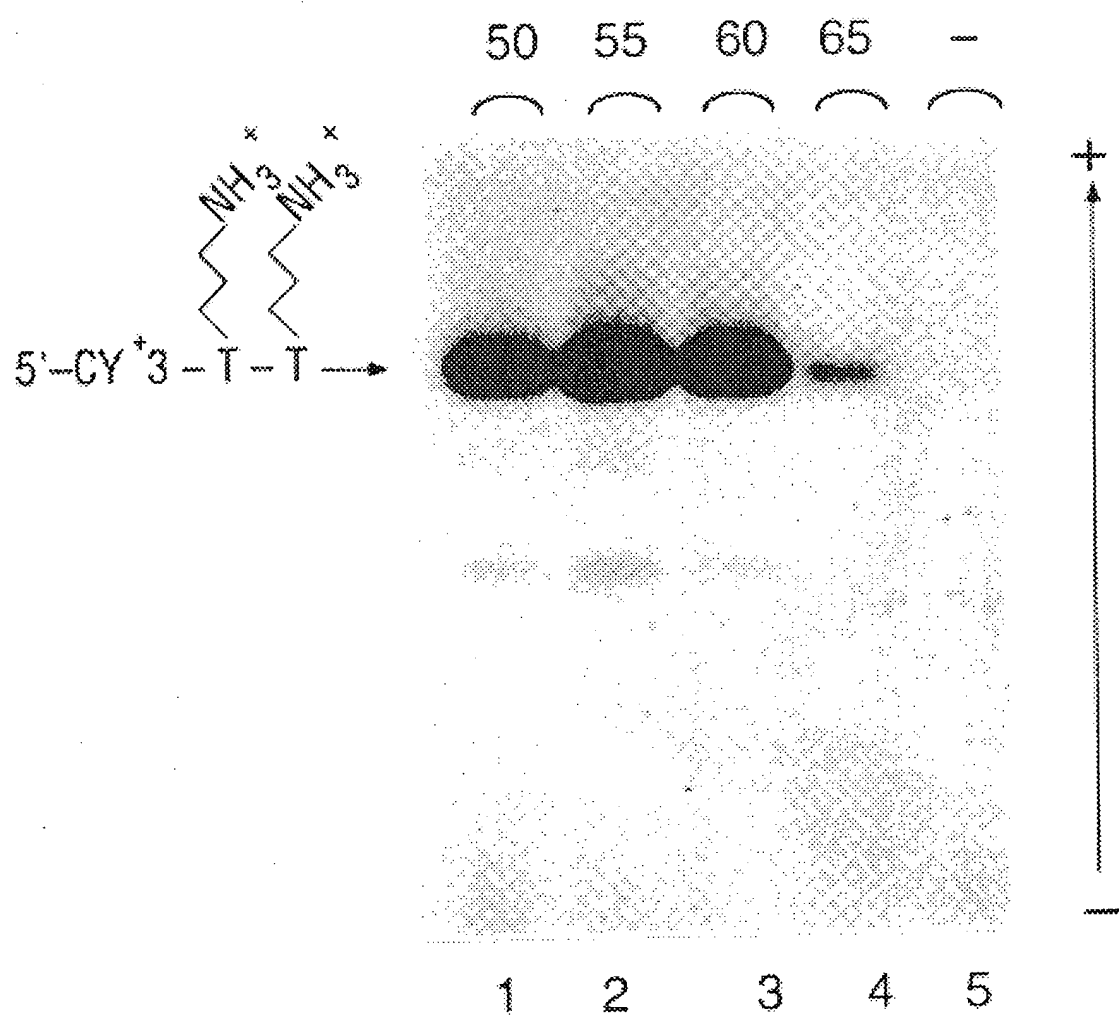


FIG. 49B

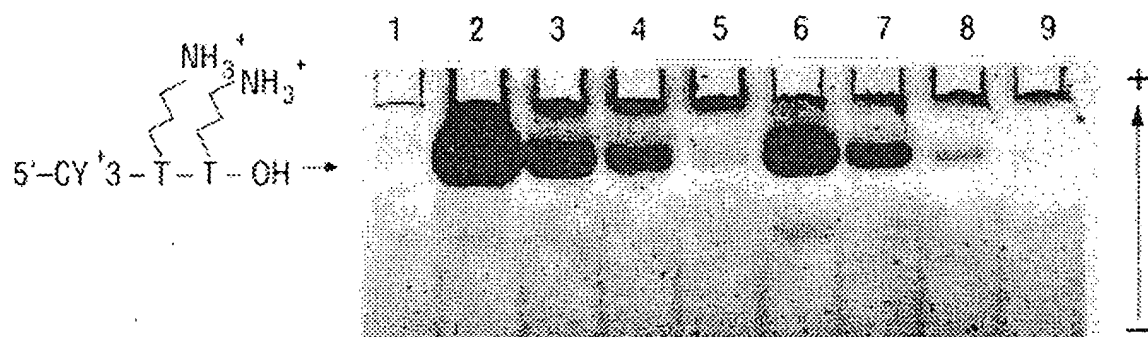


FIG. 50

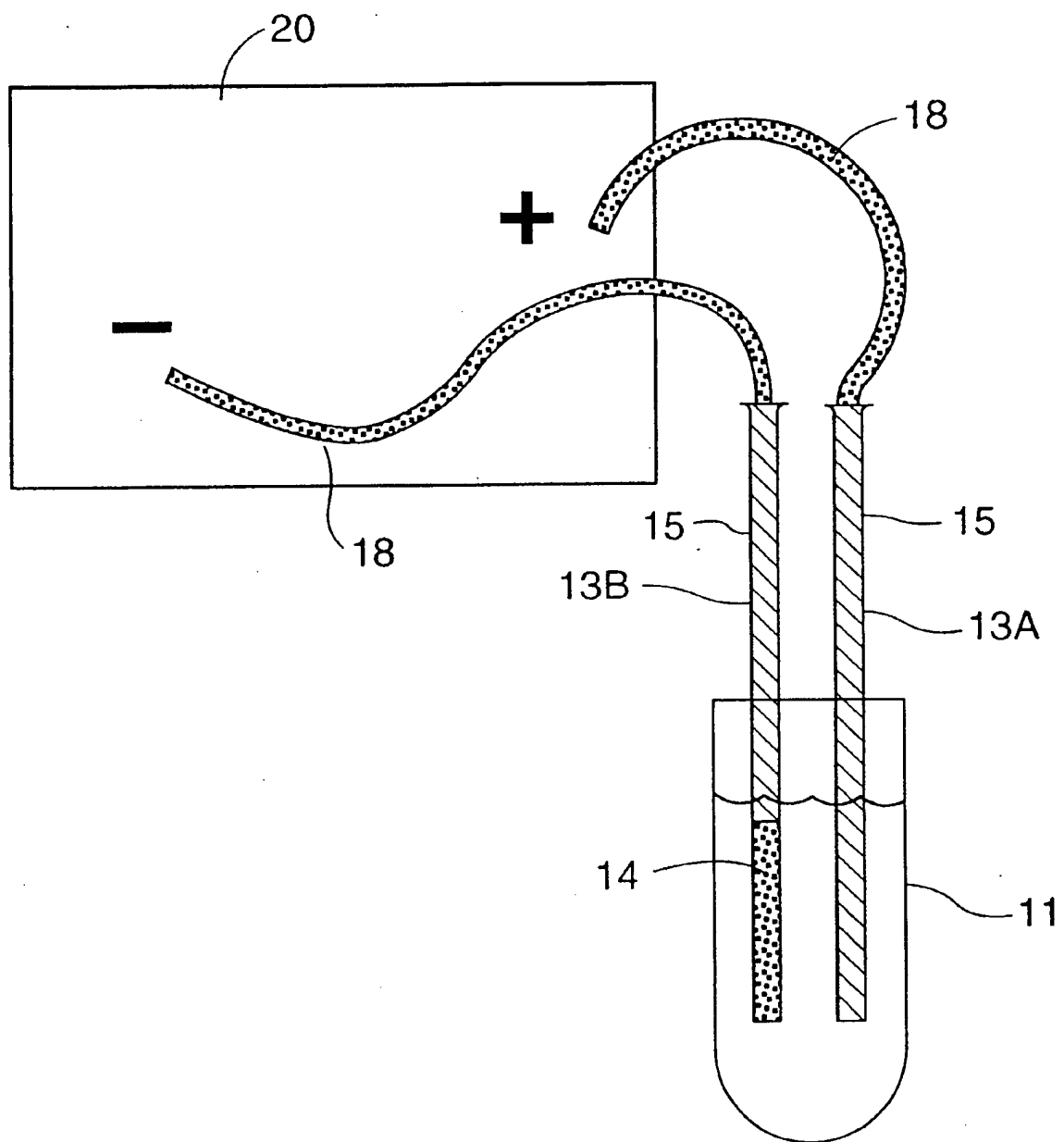


FIG. 51

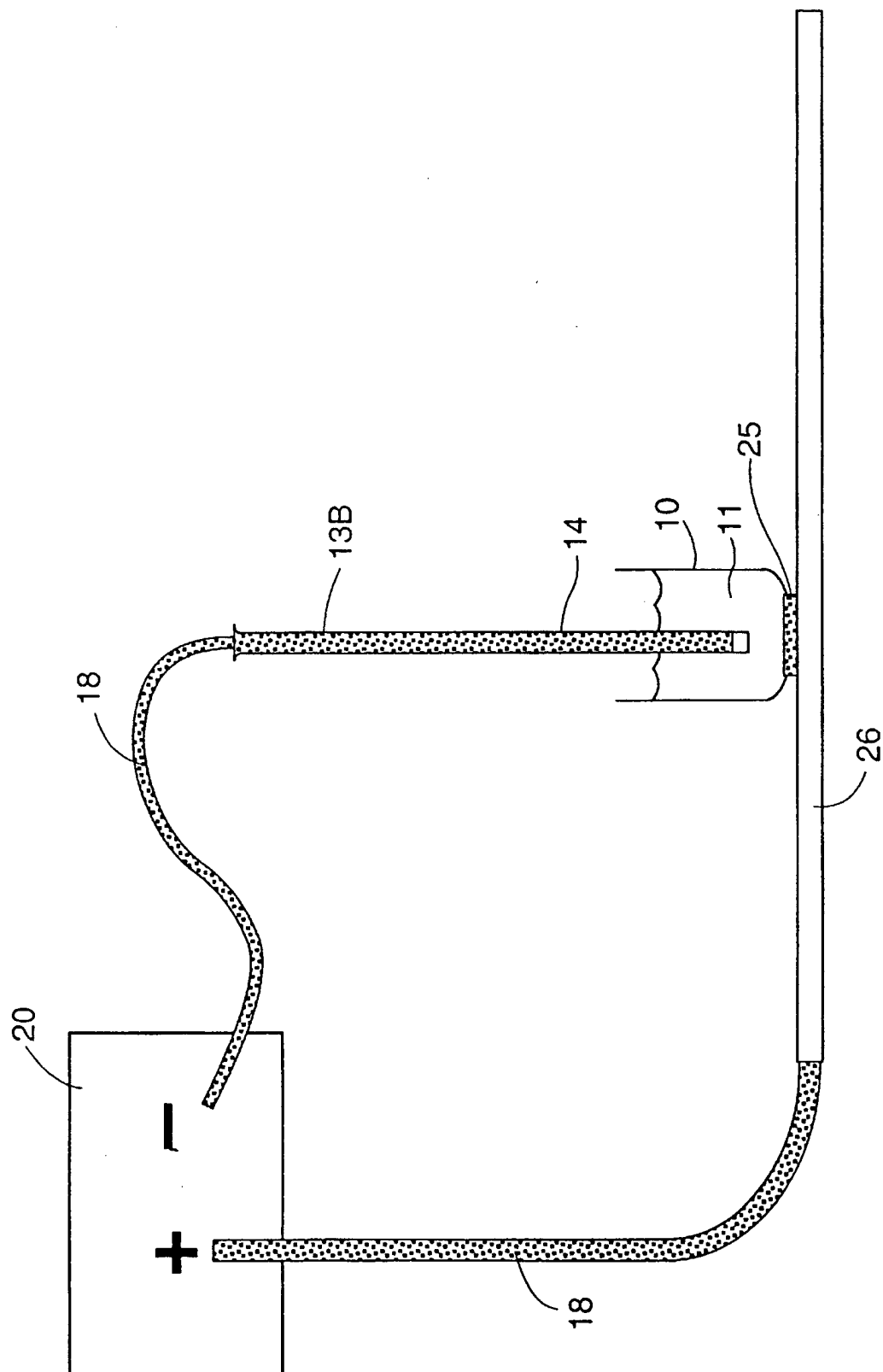


FIG. 52

PRIMER

- + C T A G

25 →

1 2 3 4 5 6

FIG. 53



FIG. 54A

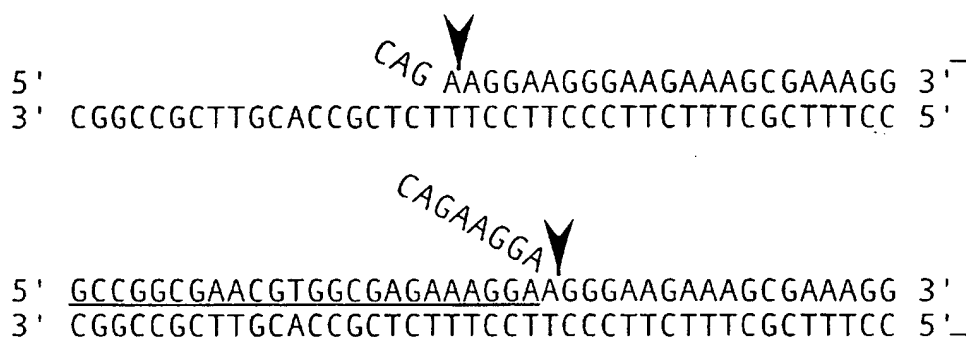


FIG. 54B

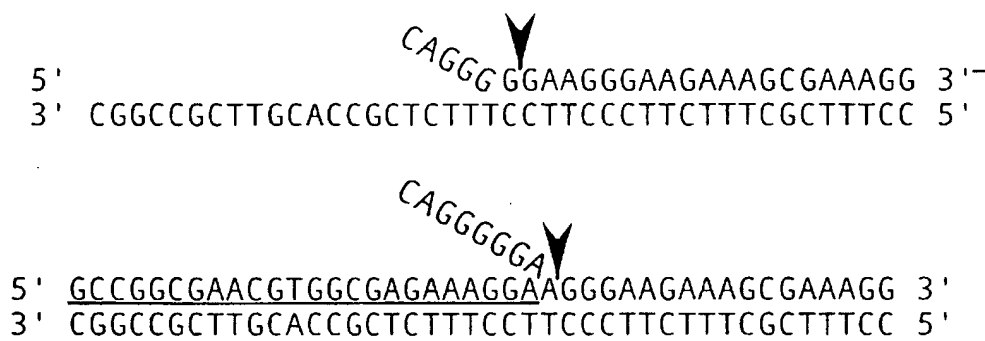


FIG. 54C

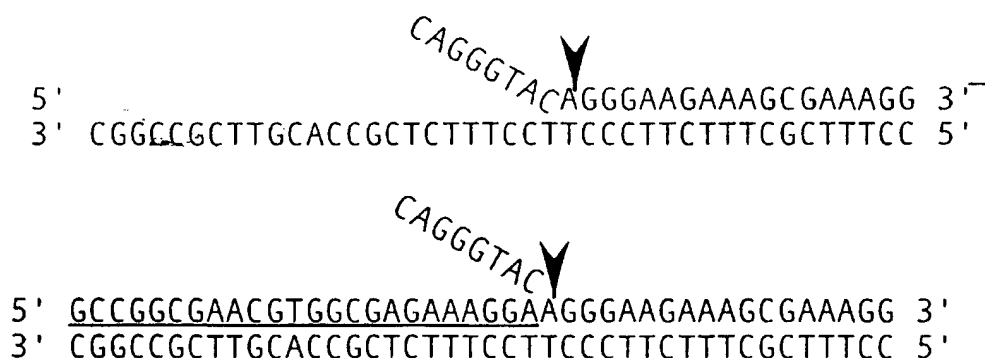


FIG. 54D

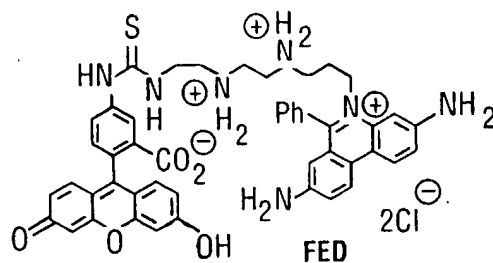
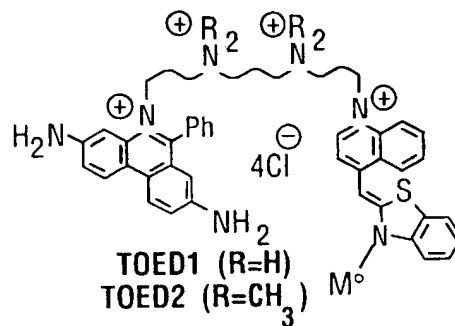
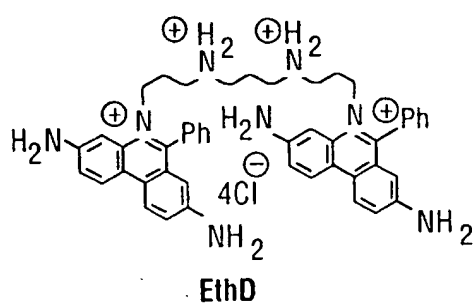
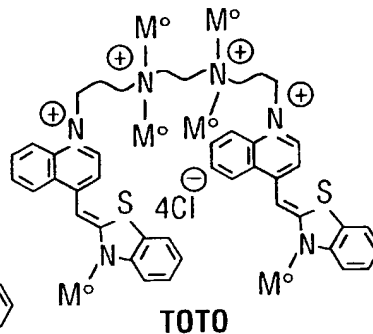
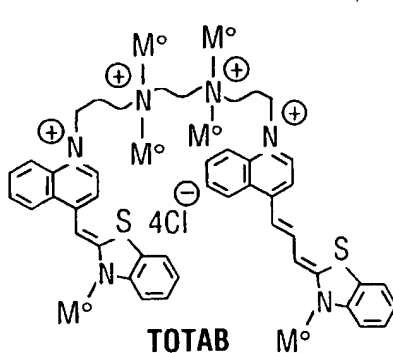
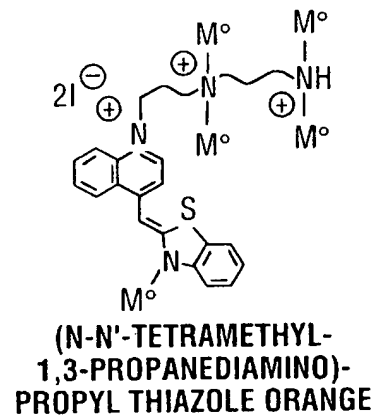
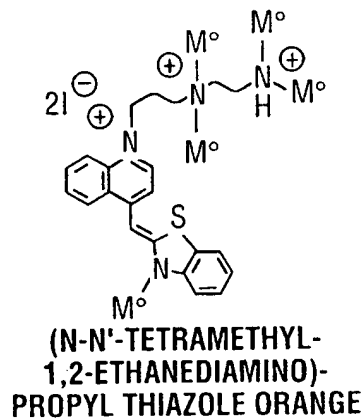
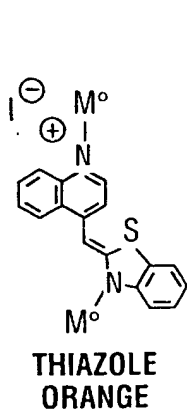
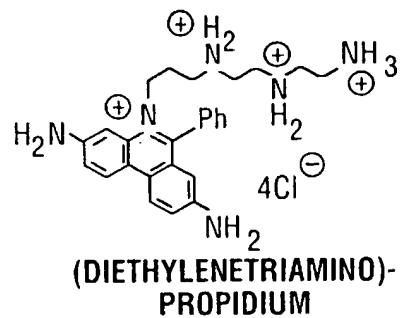
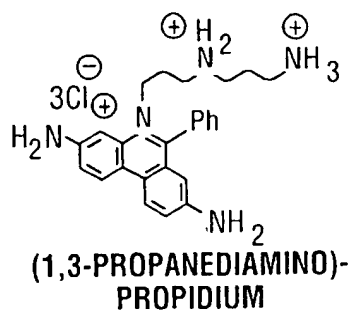
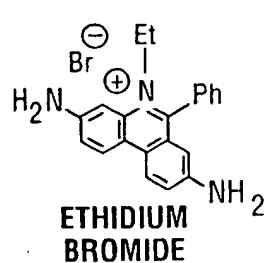
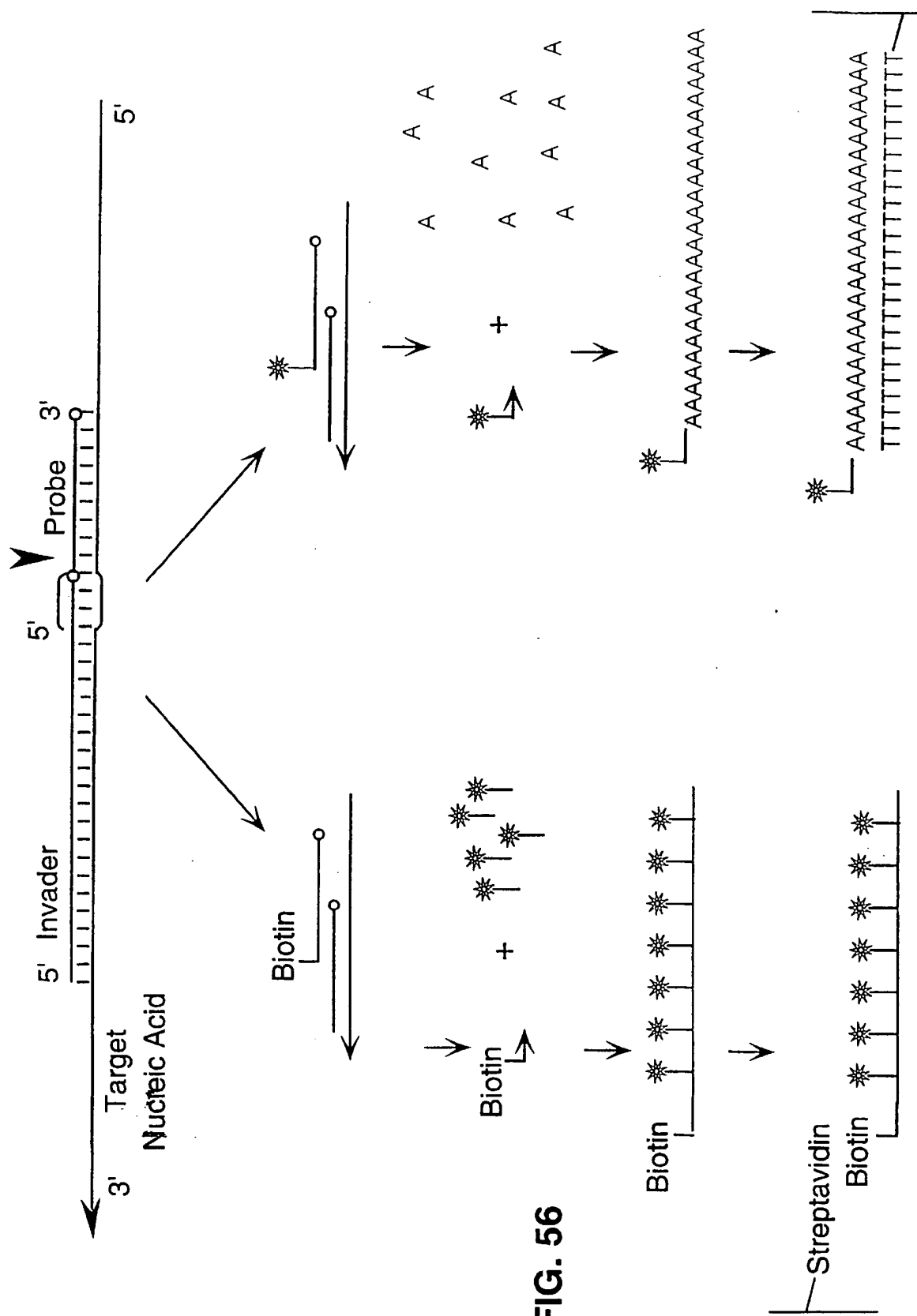


FIG. 55



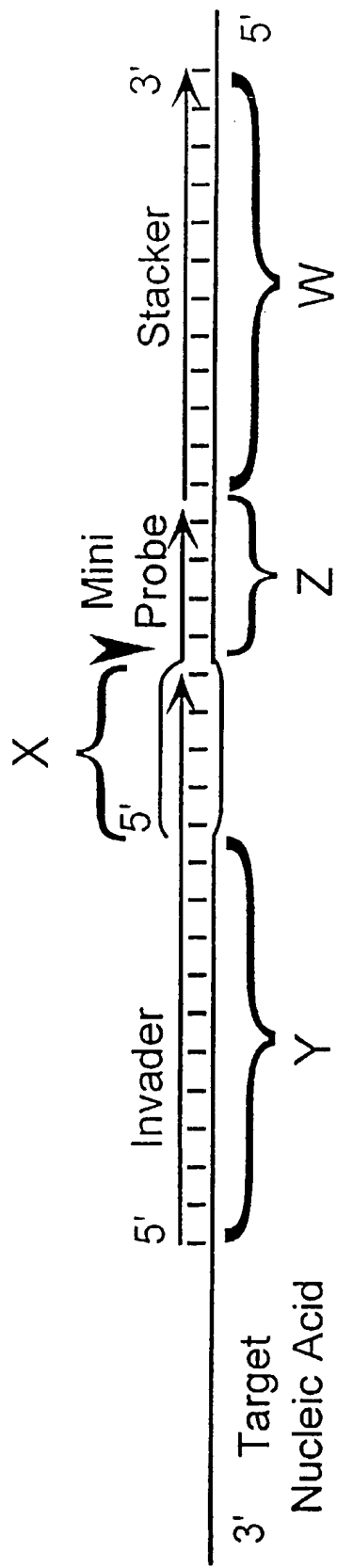


FIG. 57

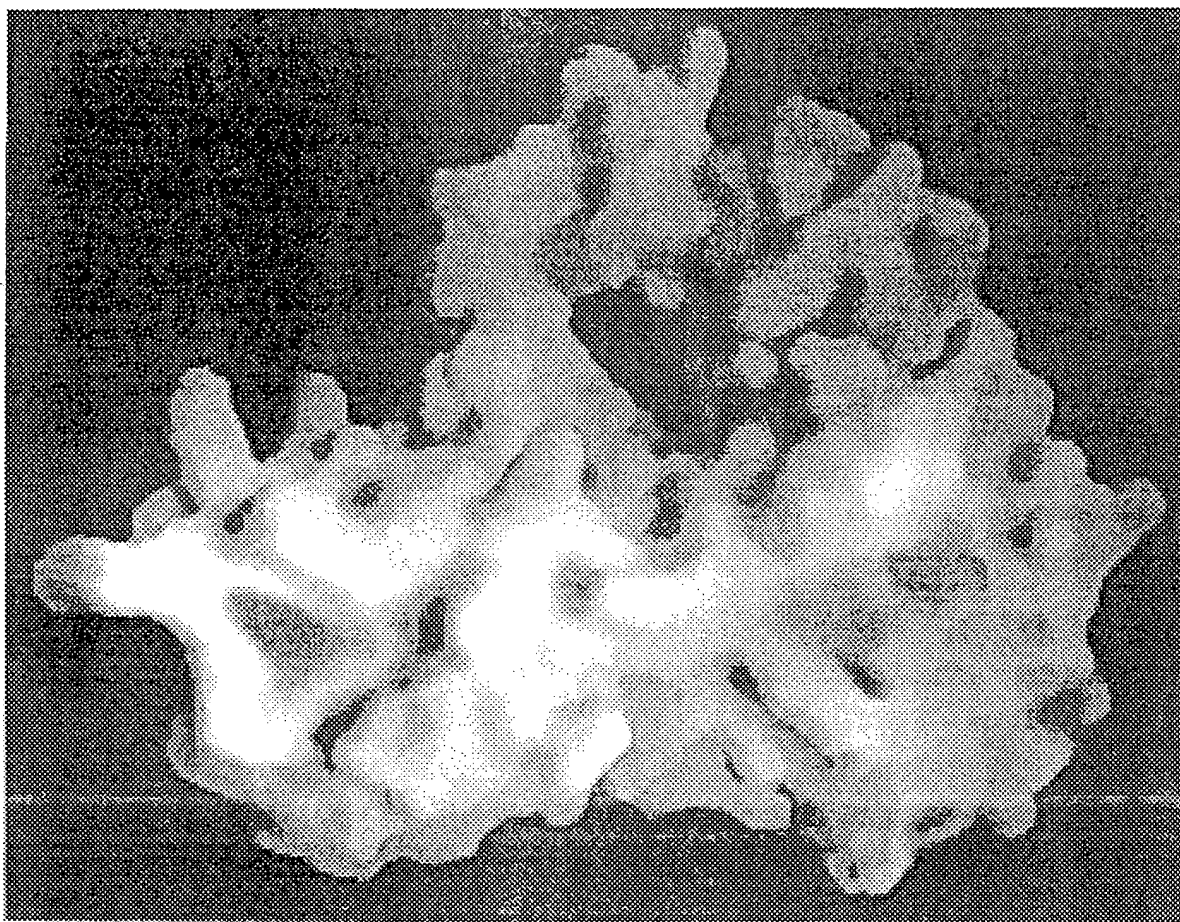


FIG. 58

	10	20	30	40	50	60	70		
1	MGVQ-----	FGDEIPK--	NIISFEDL	KGKKVAID	GMNALYQFLT	SIRLRDGS	PLNRKGEITS	AYNGVFY	MJAFEN1.PRO
1	MGVP-----	IGEIIIPR--	KEIELENL	YGKKIAIDA	LNAIYQFLST	IRQKDGTP	LMDSKGRIT	SHLSGLFY	PFUFEN1.PRO
1	MGIQGLAKLI	ADVAPSAIRE	NDIKSYFGR	KVAIDASMS	IYQFLIAVRQ	-GGDVLQNE	EGETTSHLM	GMIFY	HUMFEN1.PRO
1	MGIHGLAKLI	ADVAPSAIRE	NDIKSYFGR	KVAIDASMS	IYQFLIAVRQ	-GGDVLQNE	EGETTSHLM	GMIFY	MUSFEN1.PRO
1	MGIKGLNAII	SEHVPSAIRK	SDIKSFFGR	KVAIDASMS	LYQFLIAVRQ	QDGGQLTNE	AGETTSHLM	GMIFY	YST510.PRO
1	MGVHSFWDIAG	-----	PTARPVRL	ESLEDKRM	AVDASIWIYQFL	KAVRDQEG	NAVN-----	SHITGFFR	YSTRAD2.PRO
1	MGVSGLWNILE	-----	PVKRPVKLE	TLVNKRLA	IDASIIYQFL	KAVRDKEG	NQLKS-----	SHVVGFFR	SPORAD13.PRO
1	MGVQGLWKLE	-----	CSGROVSPE	ALEGKILAV	DISIWLNQAL	KGVDRHGN	SIEN-----	PHLLTLFH	HUMXPG.PRO
1	MGVQGLWKLE	-----	CSGHRVSPE	ALEGKVLAV	DISIWLNQAL	KGVDRSHG	NVIEN-----	AHLLTLFH	MUSXPG.PRO
1	MGVQGLWKLE	-----	CSGRPINPT	LEGKILAV	DISIWLNQAV	KGARDRQG	NAIQN-----	AHLLTLFH	XENXPG.PRO
1	MTINGIWEWANHVV	-----	RKVPNETMR	DKTLSIDG	HIWLYESLKG	CEAHHQQT	-----	PNSYLVTTFT	CELRAD2.PRO

	80	90	100	110	120	130	140		
64	KTIHLL	ENDITPIW	FDGEP	PKLKEK	TRKVRRE	MKEKAE	LKMKEAIKK-----	EDFEEAAKYAKRVSYLTP	MJAFEN1.PRO
64	RTINL	MEAGIKPV	YVFDG	EPPEFK	KKKELEK	RREAREE	AEEKWR	EALKEK-----	GEIEEARKYAQRATRVNE
70	RTIRM	MENGIKPV	YVFDG	KPPQLK	SGELAKR	SERRAE	AEKQLQQA	QAA-----	GAEQVEVEKFTKRLVKVTK
69	RTIRM	-ENGIKPV	YVFDG	KPPQLK	SGELAKR	SERRAE	AEKQLQQA	QEA-----	GMEEEVEKFTKRLVKVTK
71	RTL	MIDNGIK	PCYVFDG	KPPDLK	SHELTKR	SSRRVET	EKKLA-----	EA-----	TTELEKMKQERRLVKVS
61	RICKLL	YFGIRPV	FVFDG	GGVPVLK	RETI	RQKERRQ	KRESAK	STARKLLALQLQ	NGSNDNKRDSDVMT
61	RICKLL	FFGIKPV	FVFDG	GGAPSLK	RQTI	QKQARRL	DREENAT	VTANKLLALQ	MRHQAMLKRDAD
61	RLCKLL	FFRIRPI	FVFDG	DAPLLK	KQTLV	KRRQRKDL	ASSDSRK	TTTEKLLK	FLKRQAIKTERIA
61	RLCKLL	FFRIRPI	FVFDG	DAPLLK	KQTLA	KRRQRKDS	SASIDSR	KTTEKLLK	FLKRQALKTDRIA
61	RLCKLL	FFRIRPI	FVFDG	EAPLLK	RQTLA	KRRQRRTD	KASNDAR	KTNKLLR	FLKRQAIKAERIA
60	RIQRLLE	KIPIV	VDNINASS	SAHESK	DQNEFV	PRKRRS	FGDSPFTNLV	-----	-----

FIG. 59A

	150	160	170	180	190	200	210
130	KMVENCKYLLSL	MGIPYVEAPSEGEQA	SYMAKKGDVWAVVSQ	QDYDALLYGAPRVVRNL	TTTKEM----	MJAFEN1.PRO	
130	MLIEDAKKLL	ELMGIPVQAPSEGEQA	QAAYMAAKGSVYASASQ	QDYDSLFLGAPRLVRNL	ITGKRKLPGK	PFUFEN1.PRO	
136	QHNDCKHLLSL	MGIPYLDAPSEAEASCAAL	VKAGKVYAAATEDMDCL	TFGSPVLMRHLTASEAKKLPIQ		HUMFEN1.PRO	
134	QHNDCKHLLSL	MGIPYLDAPSEAEASCAAL	AKAGKVYAAATEDMDCL	TFGSPVLMRHLTASEAKKLPIQ		MUSFEN1.PRO	
134	EHNEEAQKLLGL	MGIPYIIAPTEAEQAELAK	KGKVYAAASEDMDTLCYRTPFL	RHLTFSEAKKEPIH		YST510.PRO	
131	DMIKEVQELL	SRFGIPYITAPMEAEQAEL	QLNLVDGIIITDSDVFL	FGGKIYKNMFHEKNY----	VE	YSTRAD2.PRO	
131	VMIKECQELL	RLFGIPYIVAPOEAEQA	CSKLELKLVDGIVTDDSDVFL	FGGTRVYRNMFNQKF----	VE	SPORAD13.PRO	
131	QMFLESQELL	RLFGIPYIQAPMEAEQA	CAILDLTQDTSGTITDSDIWL	FGARHVYRNFNKNKF----	VE	HUMXPG.PRO	
131	QMFLESQELL	RLFGVPYIQAPMEAEAO	CAVLDLSDQTSGTITDSDIWL	FGARHVYKNFFNKNKF----	VE	MUSXPG.PRO	
131	QMCLESQELL	QLFGIPYIVAPMEAEQA	CAILDLTQDTSGTITDSDIWL	FGARHVYKNFFSQNH----	VE	XENXPG.PRO	
111	DHVYKTNALL	TELGIKVIAPGDGEAQ	CARLEQLQGVTSGCITTD	DFDYFLFGGKNLYRFD	TAGT-----	CELRAD2.PRO	

	220	230	240	250	260	270	280
195	-----PELIELNEVLED	LRISLDDLIDIAIFMGTDYN	PGGV--K--GIGFKRAYEL	VRSGVAK--DV	MJAFEN1.PRO		
200	NVYVE-IKPELII	LEEVLKELKTREKLIELAIL	VGTDYNPGGI--K--GIGLKKALE	IVRHSKDPLAKF	PFUFEN1.PRO		
206	EFHLSRILQEL	GLNQEQFVDCIILGSDYCES	IRGIGPKRAVDLIQK--HKSIEEIVRRLDPN----	KEY	HUMFEN1.PRO		
204	EFHLSRVLQEL	GLNQEQFVDCIILGSDYCES	IRGIGAKRAVDLIQK--HKSIEEIVRRLDPS----	KEY	MUSFEN1.PRO		
204	EIDTELVLRLGLDL	TIQQFVDCIMLGCDYCES	IRGVGPVTALKIKT--HGSIEKIVEFIESGESNNTKW		YST510.PRO		
198	FYDAESI	KLGLDRKNMIELAQLLGSDYT	NGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNGO	FDKRK	YSTRAD2.PRO		
198	LYLMDDMKREF	NVNQMDLIKLAHLLGSDYTMGLSRVGPVLA	EILHEFPDGTGLFEFKWFORLSTGHAS		SPORAD13.PRO		
198	YYQYVDFHNQ	GLDRNKLINLAYLLGSDYTEG	IPTVGCVTAMEILNEFPGHGLEPLLKFSEWHEAQKNP		HUMXPG.PRO		
119	YYQYVDFYSQ	GLDRNKLINLAYLLGSDYTEG	IPTVGCVTAMEILNEFPGRGLDPLLKFSEWHEAQNNK		MUSXPG.PRO		
198	YYQYADIHNOL	GLDRSKLINLAYLLGSDYTEG	IPTVGVVVSAMEILNEFPQGQGLEPLVKFKEWSEAQKDK		XENXPG.PRO		
175	-----	-----	-----SSTACLDHIMHLSLGRMF	-----	CELRAD2.PRO		

FIG. 59B

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKKIFKEPKV-----	TD--	NYSLSLKL	PDKEGI	IKFLVD	ENDFN	YD MJAFEN1.PRO
265	QKQSDVDLYAIKEFFLNPPV-----	TD--	NYNLVWRD	PDDEEG	ILKFLC	DEHDF	SEE PFUFEN1.PRO
269	PVPENWLHKEAHQLFLEPEV-----	LDPE	VELKWSE	PNEEEE	LIKFMCG	EKFSEE	HUMFEN1.PRO
267	PVPENWLHKEAQQLFLEPEV-----	VDPE	VELKWSE	PNEEEE	LVKFMC	GKQFSEE	MUSFEN1.PRO
272	KIPEDWPYKQARMLFLDPEV-----	IDGNE	INLKWSP	PKKEKE	LIEYLC	DDKKF	SEE YST510.PRO
265	QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDLMLRSFMKTQLGWPHE	YSTRAD2	.PRO				
268	KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGI	PDDEL	RQFLMAT	VGWSKQ			SPORAD13.PRO
268	KIRPNPHDTKVKKKL--RTLQLTPGFPNPAAVEAYLKPVVDDSKGSFLWGK	PDLDK	IREFC	QRYFG	WNRT		HUMXPG.PRO
268	KVAENPYDTKVKKKL--RKLQLTPGFPNPAAVADAYLRPVVDDSRGSFLWGK	PDVDK	IREFC	ORYFG	WNRM		MUSXPG.PRO
268	KMRPNPNDTKVKKKL--RLLDLQQSFNPAAVASAYLKPVVDESKSAFSWGR	PDLEQ	IREFC	ESRFG	WYRL		XENXPG.PRO
194	-----EKKVSRPHLISTAILLGCDYFORGVQNI	GIVSVF	-ILGE	FDDG	NEEID	PHVILDR	FASYVRE CELRAD2.PRO

	360	370	380	390	400	410	420	
300	RVKKHVDKLYNLIA-----						MJAFEN1.PRO	
314	RVKNGLERLKKAI-----						PFUFEN1.PRO	
320	RIRSGVKRLSKSRQGS-TQGRLD	DDFFKVT					HUMFEN1.PRO	
318	RIRSGVKRLSKSRQGS-TQGRLD	DDFFKVT					MUSFEN1.PRO	
323	RVKSGISRLKKGLKSG-IQGRLD	GFFOVV					YST510.PRO	
335	KSDEILPLIRDVNKRKK-----						KGKQ YSTRAD2.PRO	
337	RTNEVLLPVIQDMHKKOF-----						VGTV SPORAD13.PRO	
336	KTDESLFPVLKQLDAQQTQLRID	SFFRLAQ	QEKEDAK	RIKSQ	RNLRA	VTCMLR	KEKEAA	SEIEAVSVAM HUMXPG.PRO
336	KTDESLYPVLKHLNAHQTLRID	SFFRLAQ	QEKQDA	KLKSH	RLSRA	VTCMLR	KERE	EKAPELTKVTEAM MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQTQLRID	SFFRLAQ	HEAAG--	--LKS	QRLRA	VTCMLR	KERD	VEAEEVEAAVAM XENXPG.PRO
257	EIPARSED	TQRKLRLRR	KKYNFP	VGFPNC	DAVHNA	ITMYLR	PPVSSE	IPKIIPR-----AANFQQVAEIM CELRAD2.PRO

FIG. 59C

	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----GSL	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----GSL	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----PK-T	YST510.PRO
357	KRINEFF	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	SNLTQFFEGGNTNVYAPRVAYHFKSKRLENALSSFKNQISNQSPMSEEEIQADADAFGESKGSDELOSRIL	SPORAD13.PRO					
406	EKEFELDKAKRKTQKRGITNTLEESSLKRRLSDSKRNTCGGFLGETCLSESSDGSSEHAESSLM	HUMXPG.PRO					
406	EKEFELDDAKGKTOKREL PYK	-----	-----KETSVPKRRRPSGNGGFLGDPYCSESPQESSCEDGEGSSVM	MUSXPG.PRO			
403	ERECTNQRKGQKNTKS	-----	-----QGTKRKRKPTESQEDQDPGGGFIGIELKTLSSKAYSSD	XENXPG.PRO			
322	MKECGWPATRTQKELALSIRRKVHLTTTVAQTRIPDFFAATKSKNFTPIVEPCESLEDYISANN	-----	-----T	CELRAD2.PRO			

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	-----	NKTKQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	SAKRKEPEPKGST	-----	-----	-----	-----	-----	KKKAKTGAAG HUMFEN1.PRO
350	SAKRKEPEPKGPA	-----	-----	-----	-----	-----	KKKAKTGGAG MUSFEN1.PRO
354	KEQLAAAKRAQE	-----	-----	-----	-----	-----	NKKLNKNKNK YST510.PRO
364	-----	-----	-----	PREYISGDKKLNTSKRISTATGKL	-----	-----	KK YSTRAD2.PRO
429	RRKKMMASKNSSDSDSDSEDNFLASLTPKTNSSSISIENLPRKTKLSTSL	-----	-----	-----	-----	-----	KKP SPORAD13.PRO
476	NVQRRTAAKEPKTSASDSONSVKEAPVKNGGATTSSSDSDDDGGKEKMLVLTARSVFGKKRRKLRARG	HUMXPG.PRO					
469	SARQSAEESKIGCSDVPLVRDSPHGRQGCVSTSSDSEDGEDKAKTVLVTARPVFGKKRRKLSMK	MUSXPG.PRO					
458	-----	GSSSDAEDLPSGLIDKQSQSGIVGROKASNKVESSSSDDEDRTVMVTAKPVFQGGKTKSKTMKE	XENXPG.PRO				
387	WMRKRKRSESPQILQHHAKRQVPDRK	-----	-----	-----	-----	-----	RSVKIRAFKPYPTDVI CELRAD2.PRO

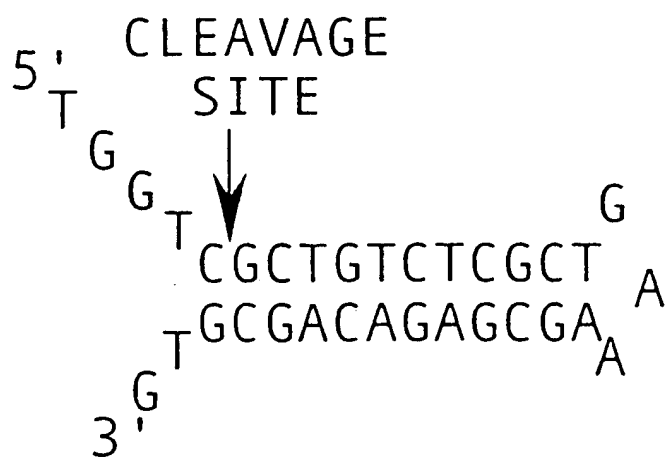
FIG. 59D

322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 ---RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

FIG. 59E

S-33



11-8-0

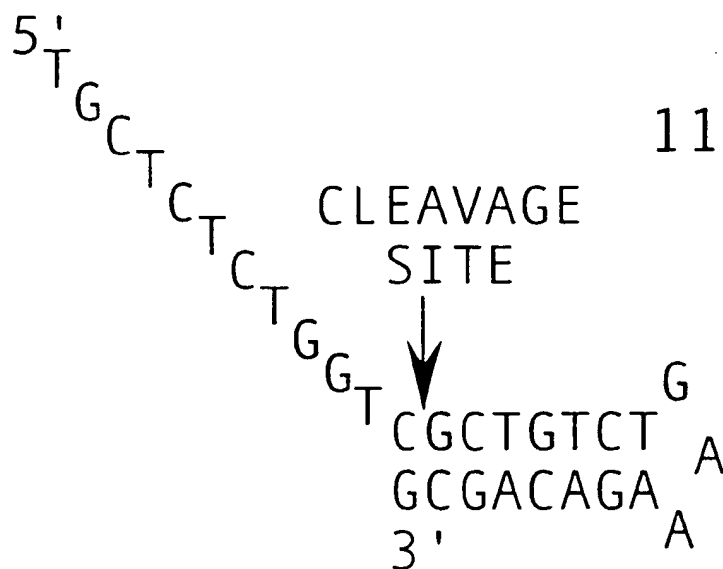


FIG. 60

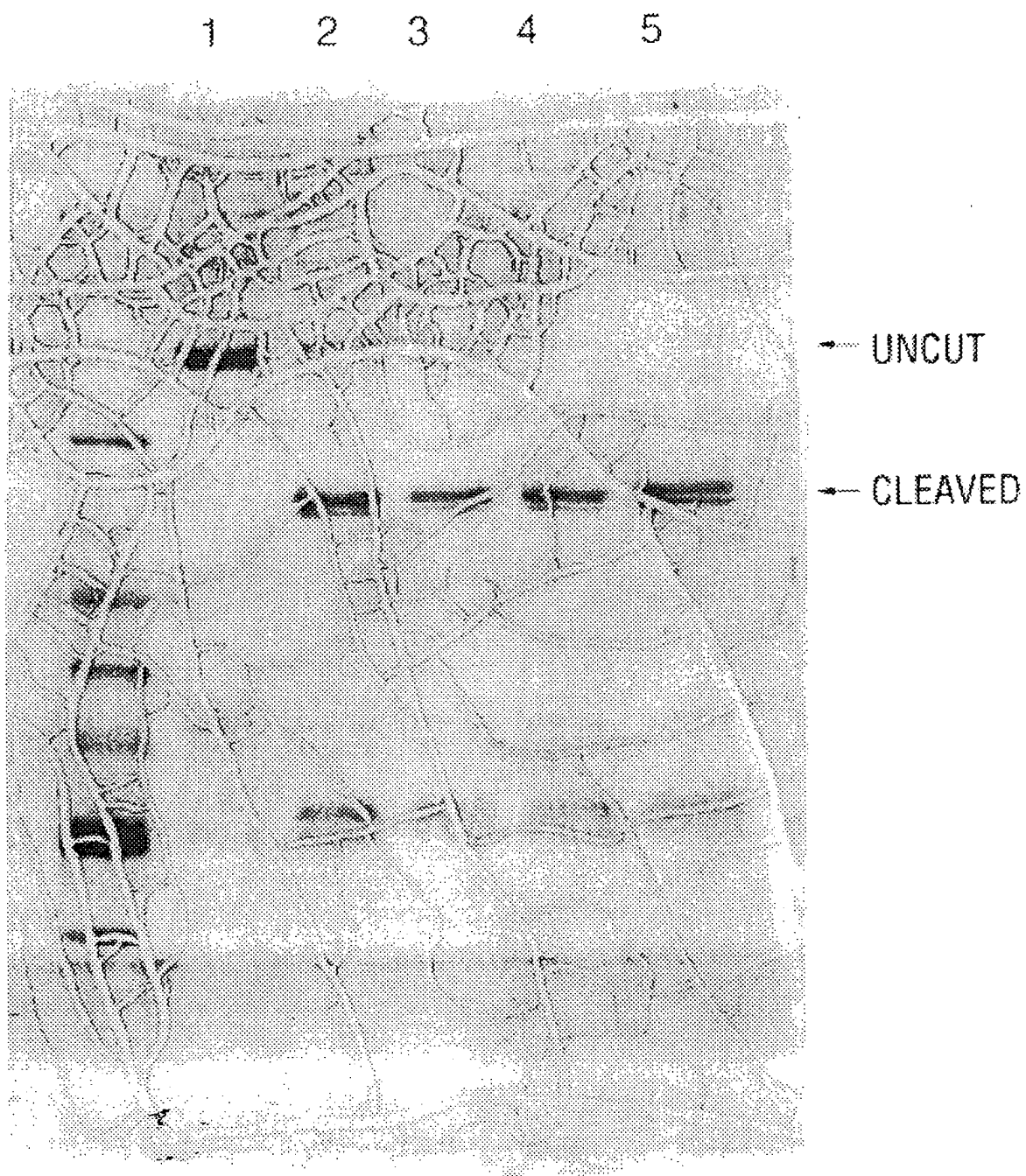


FIG. 61

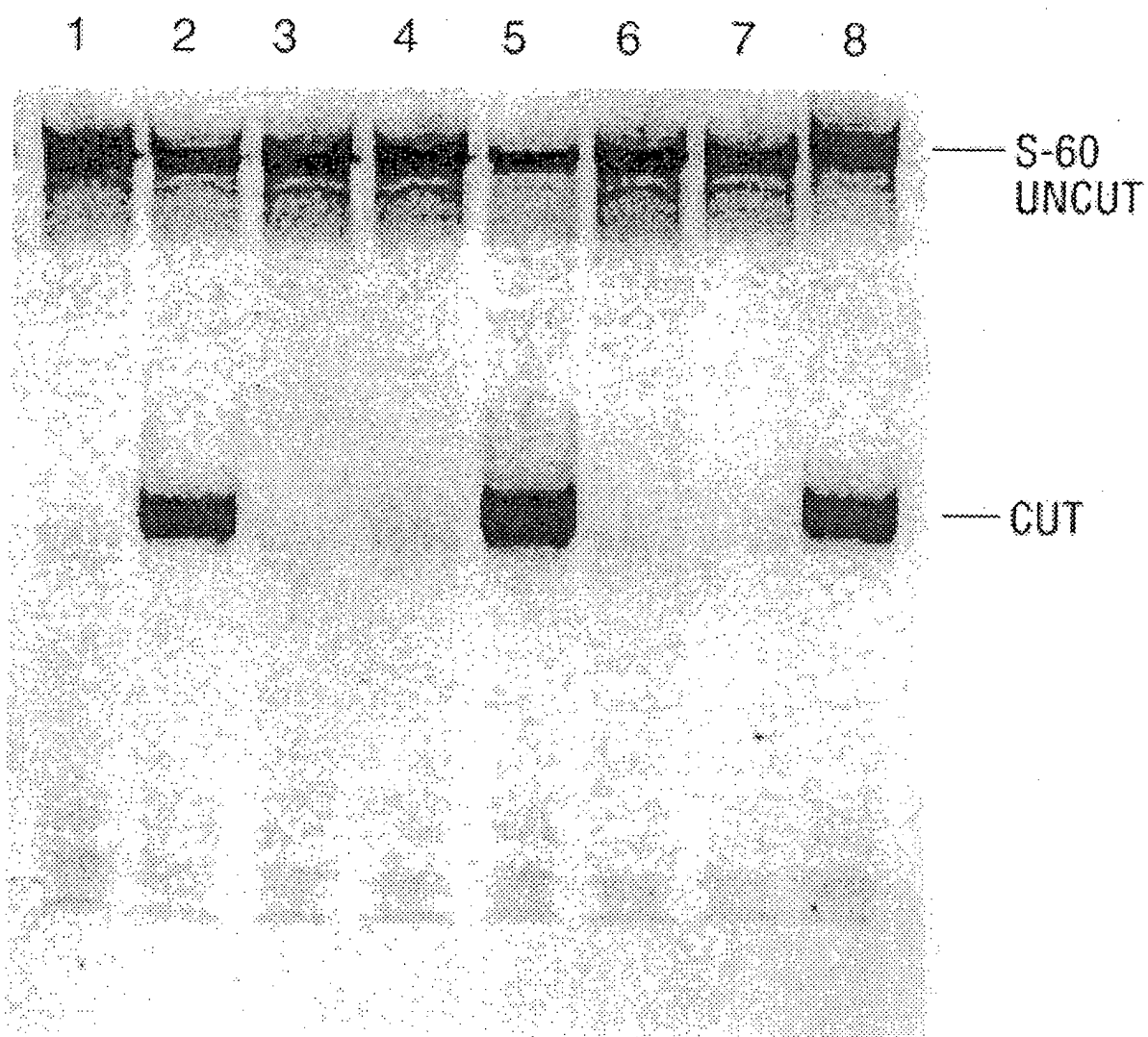


FIG. 62

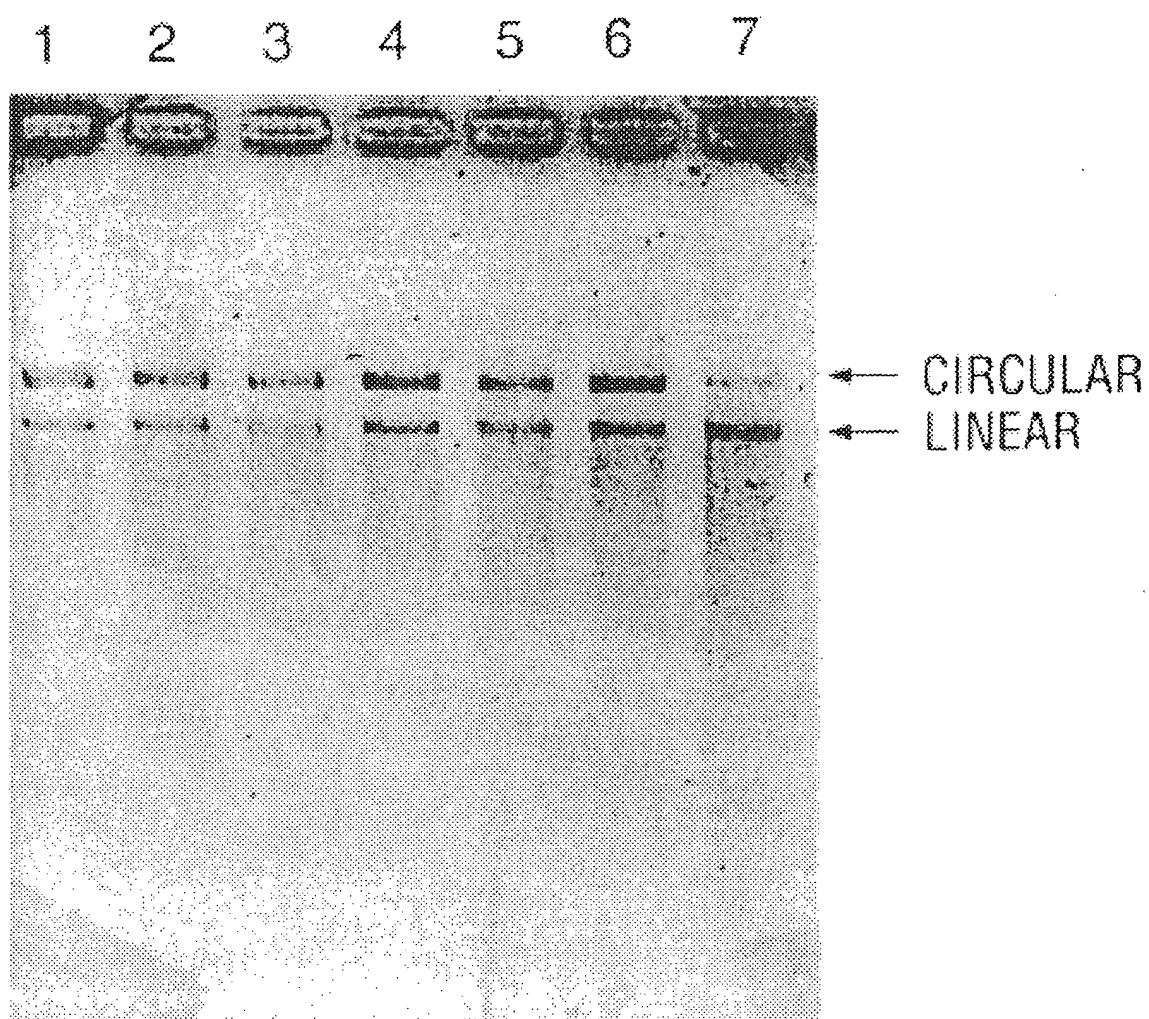


FIG. 63

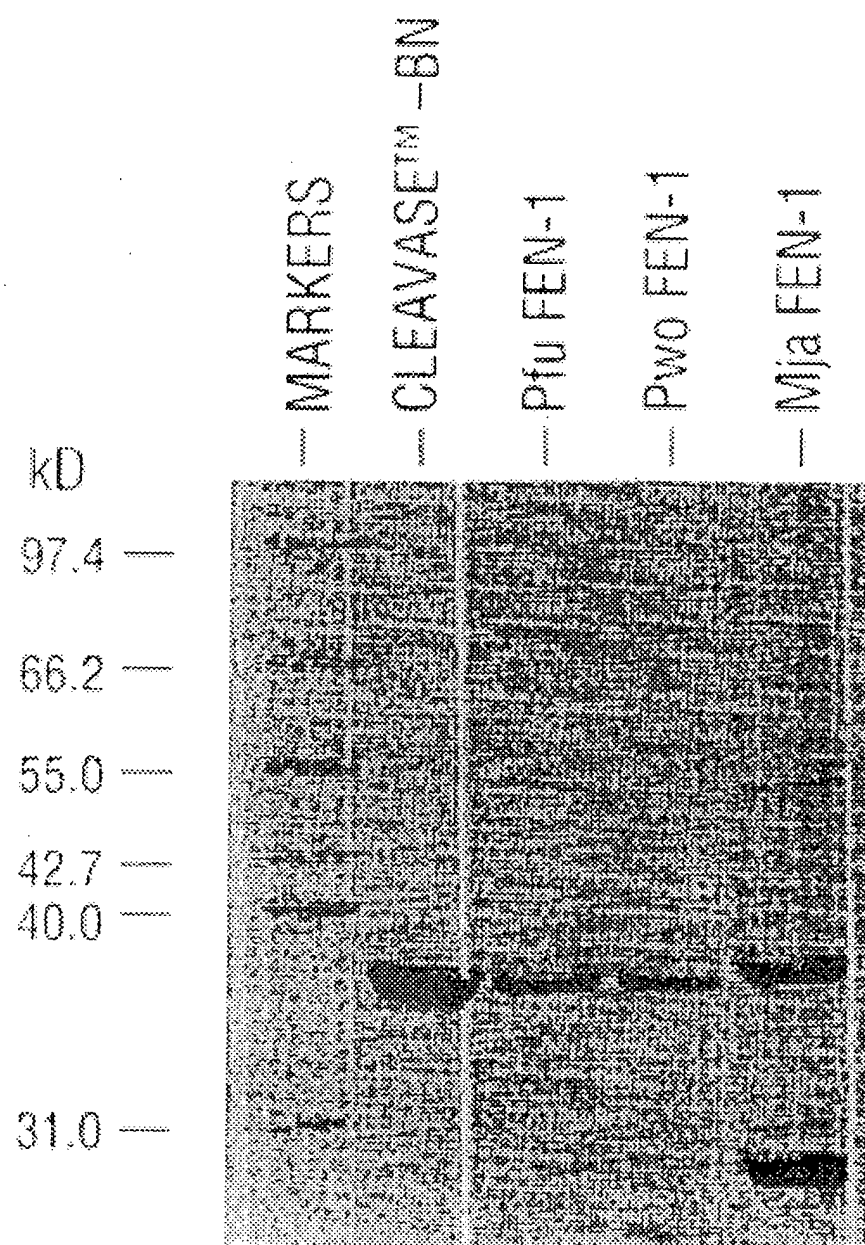


FIG. 64

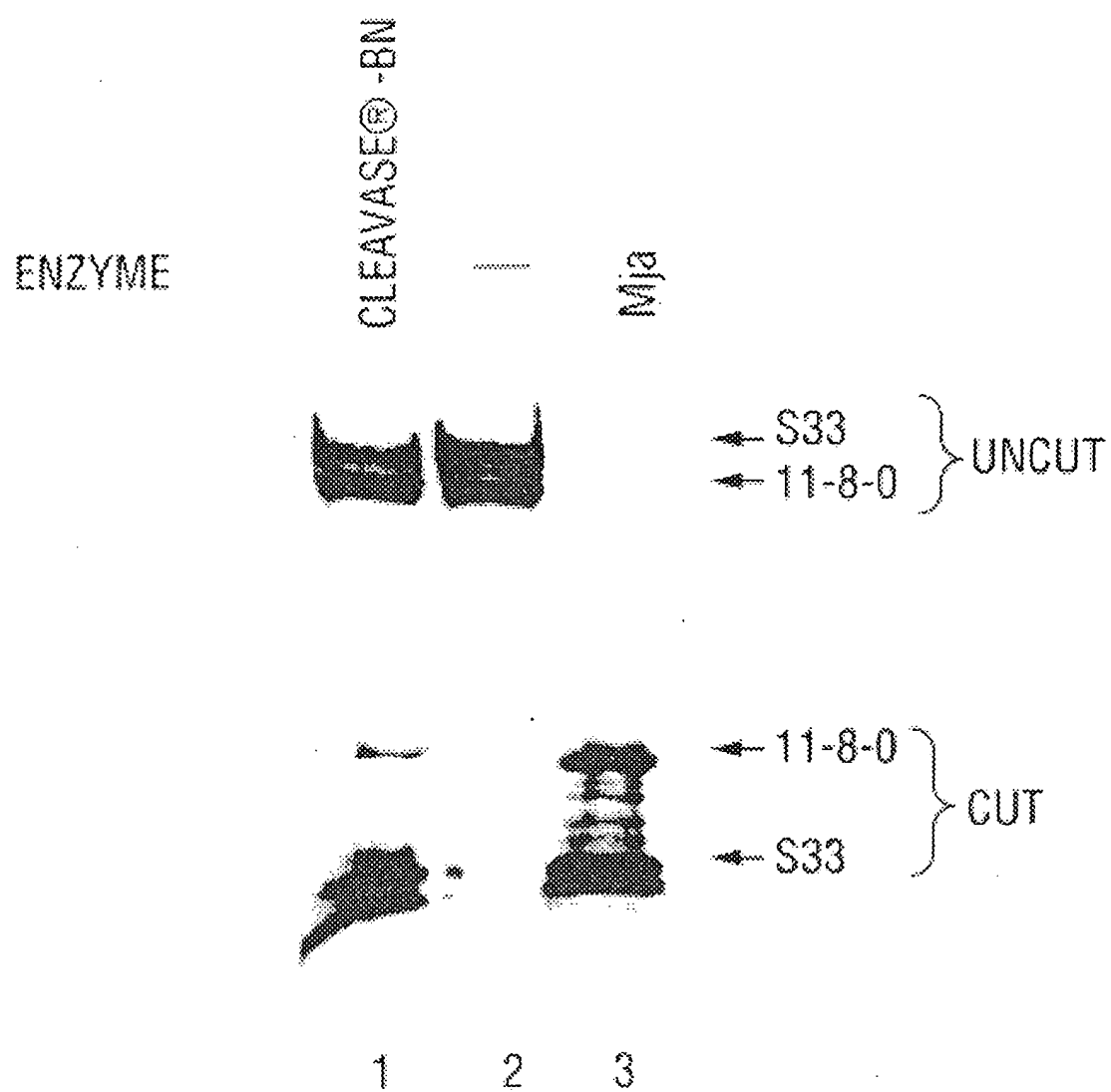


FIG. 65

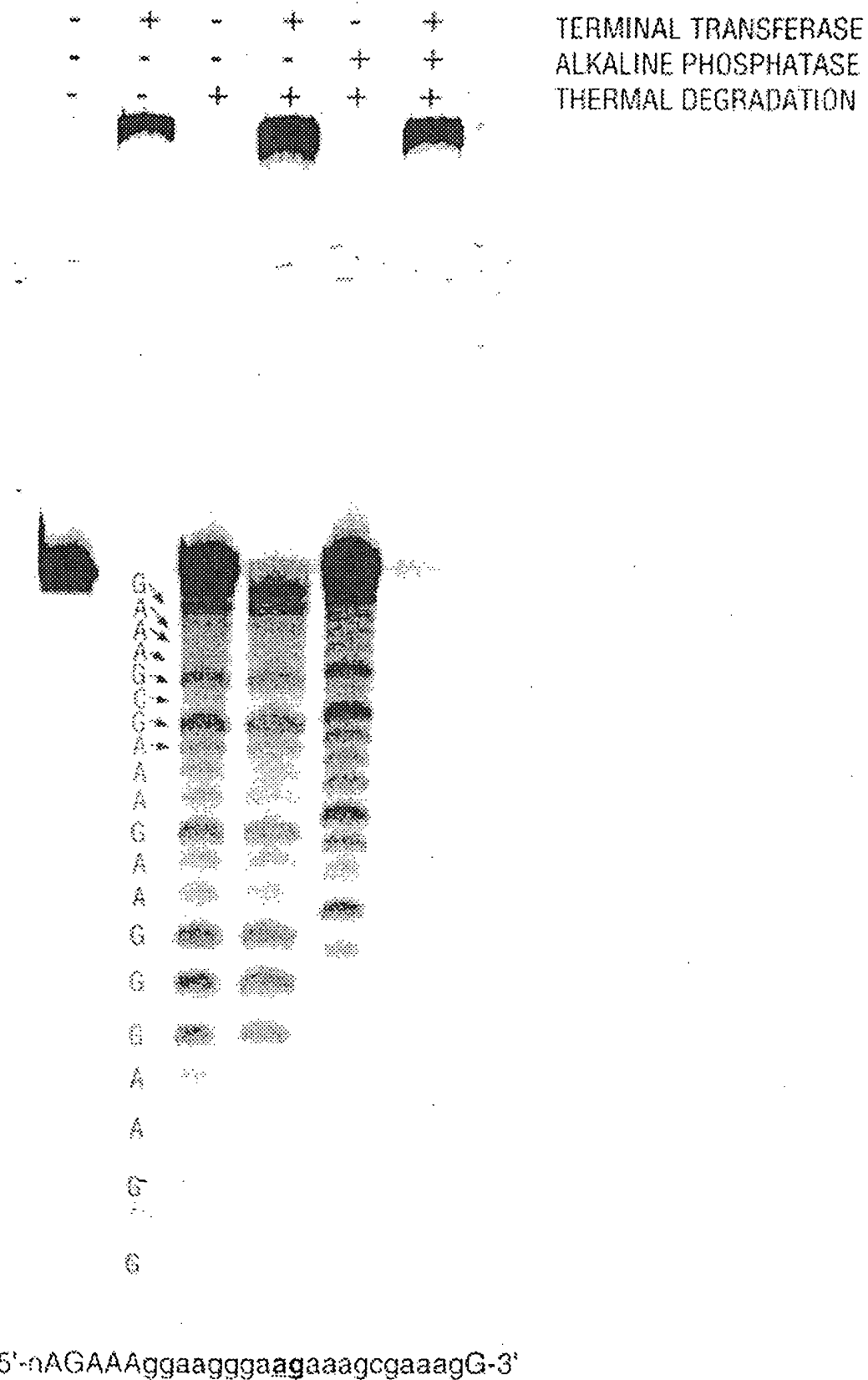


FIG. 66

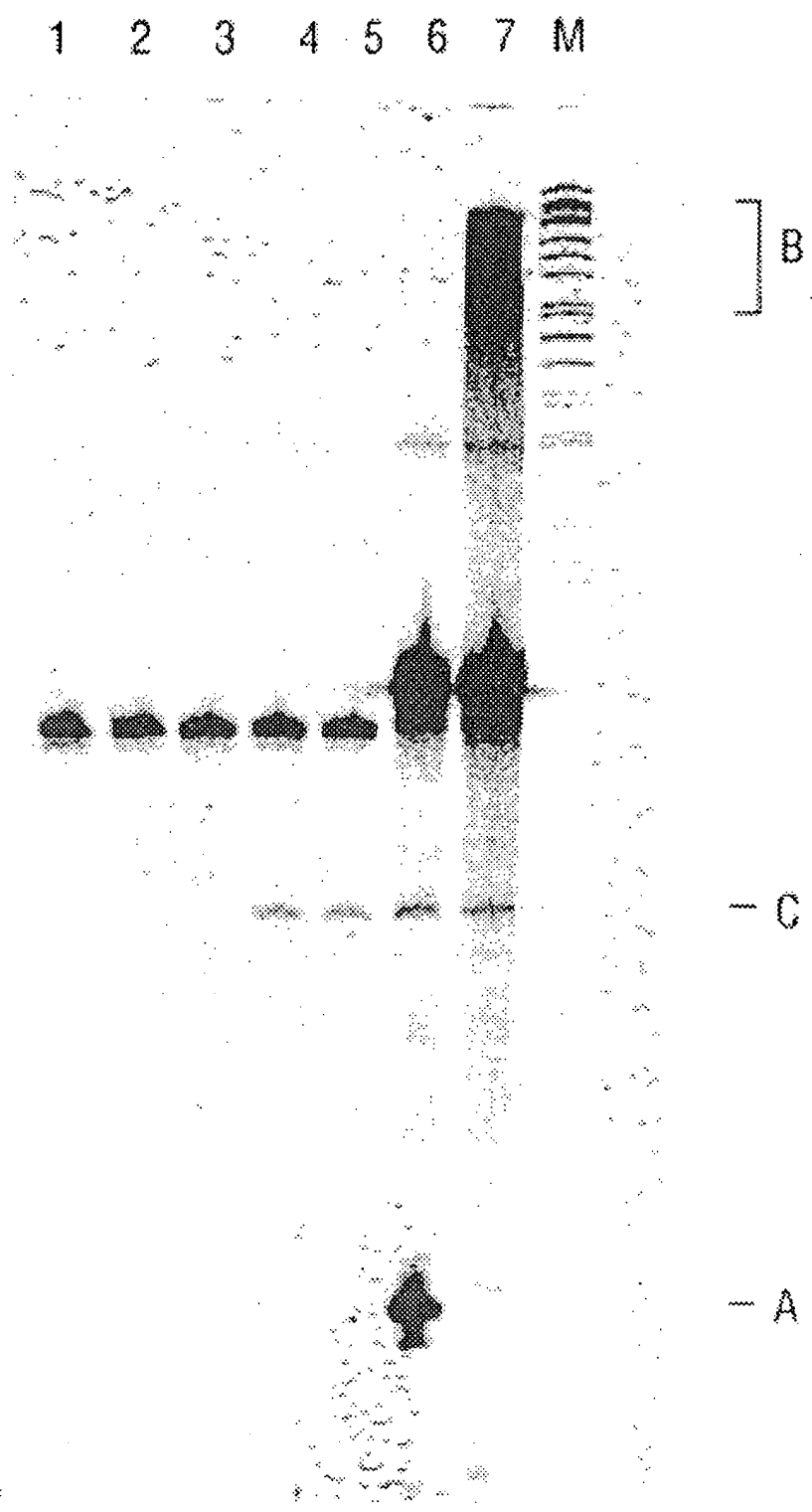


FIG. 67

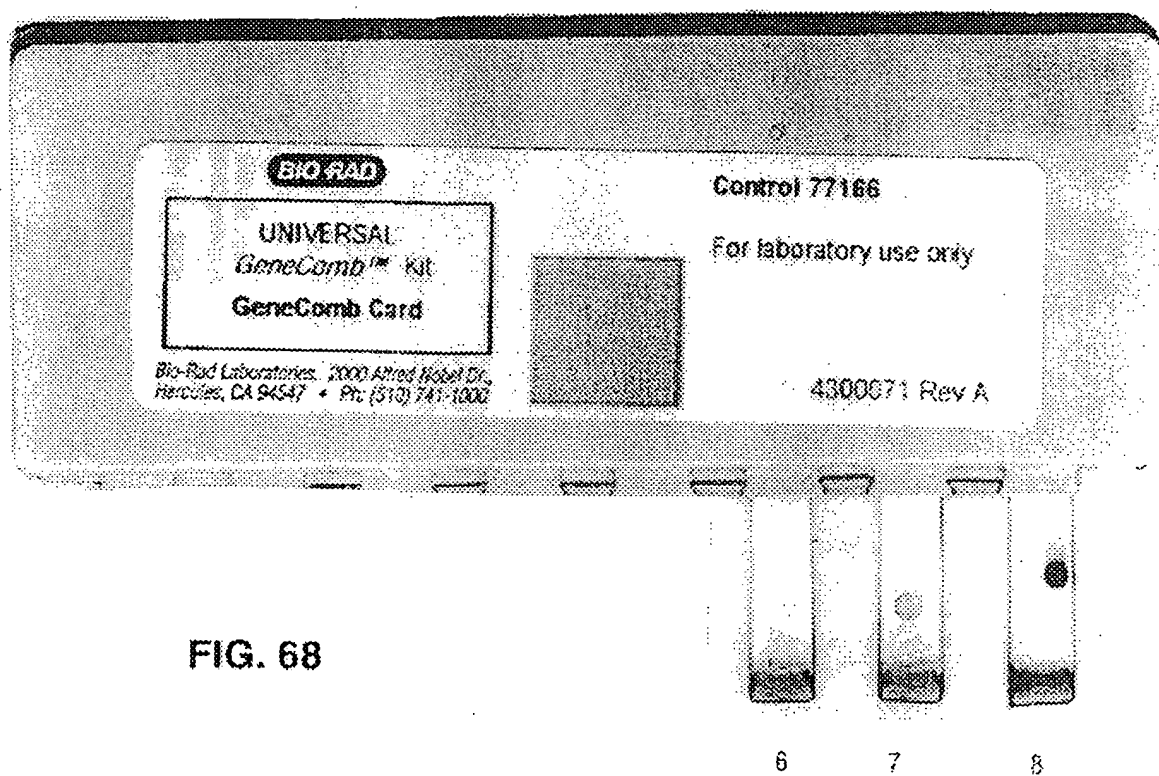


FIG. 68

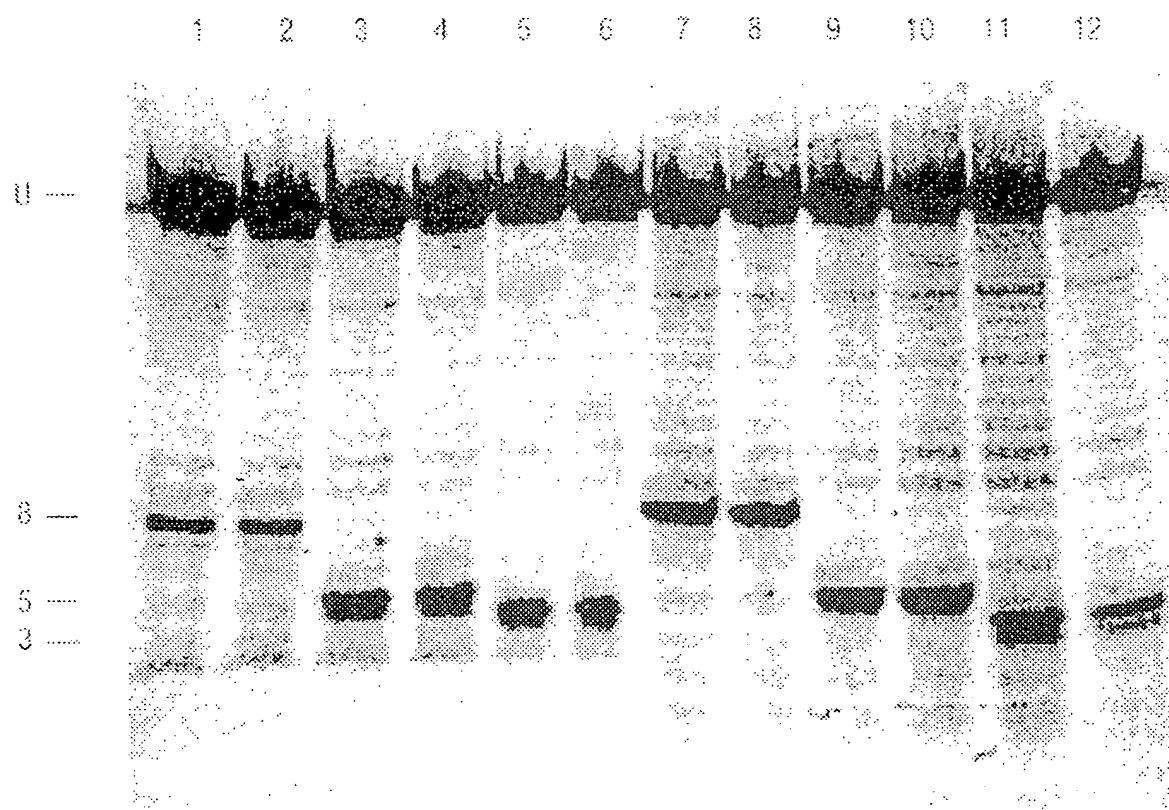


FIG. 69

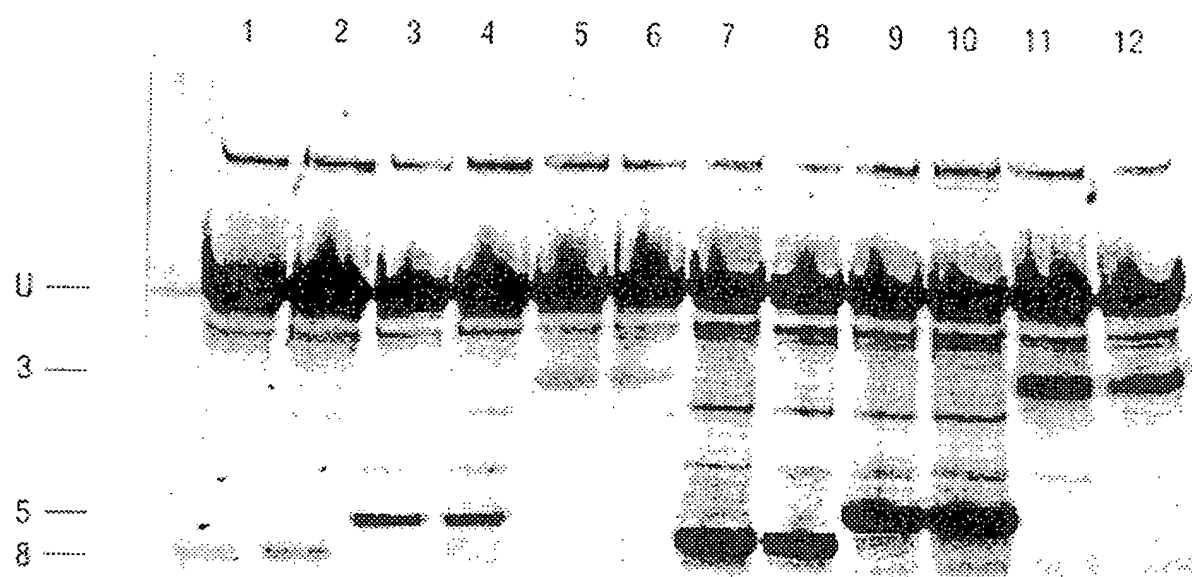


FIG. 70

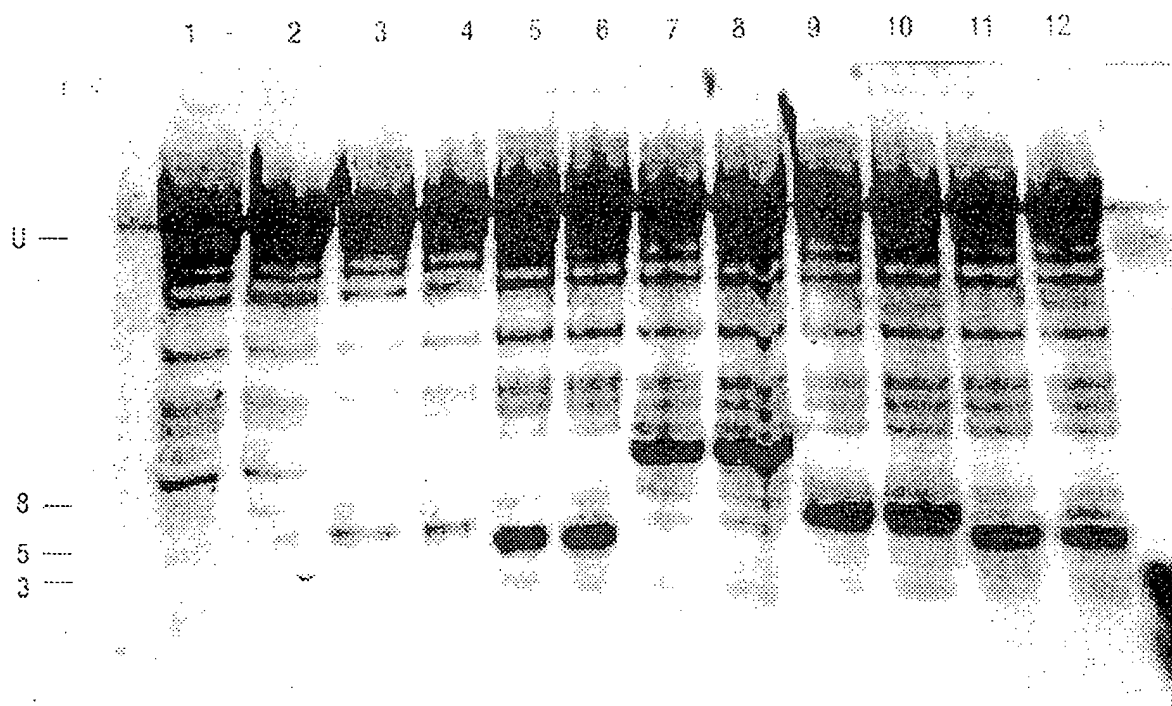


FIG. 71

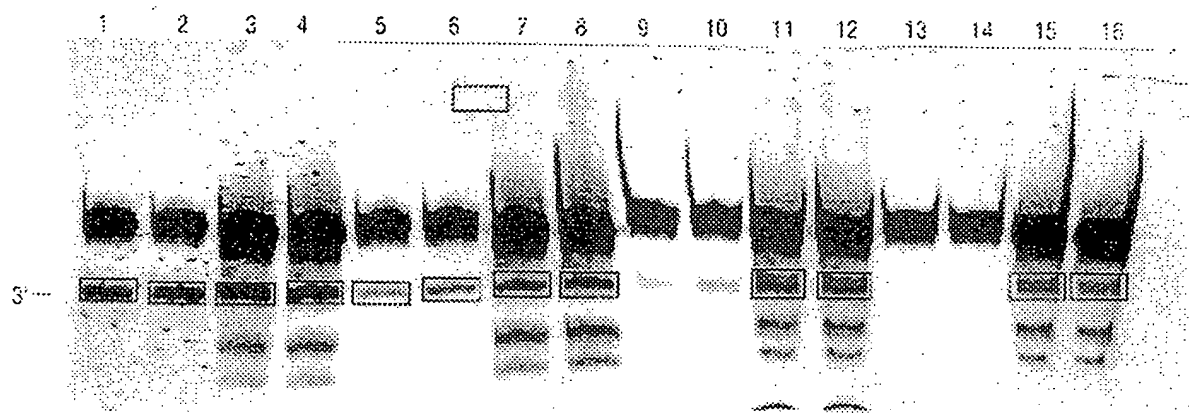


FIG. 72A

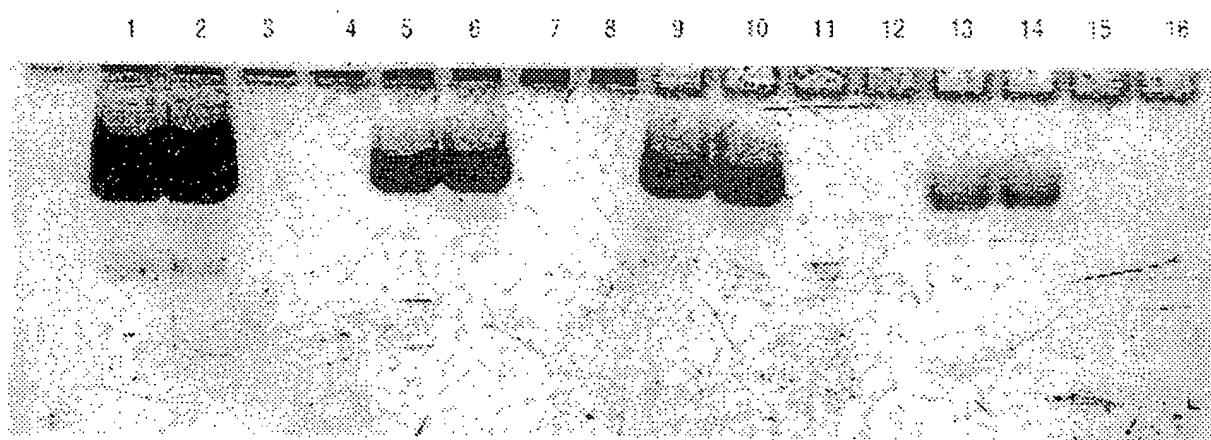
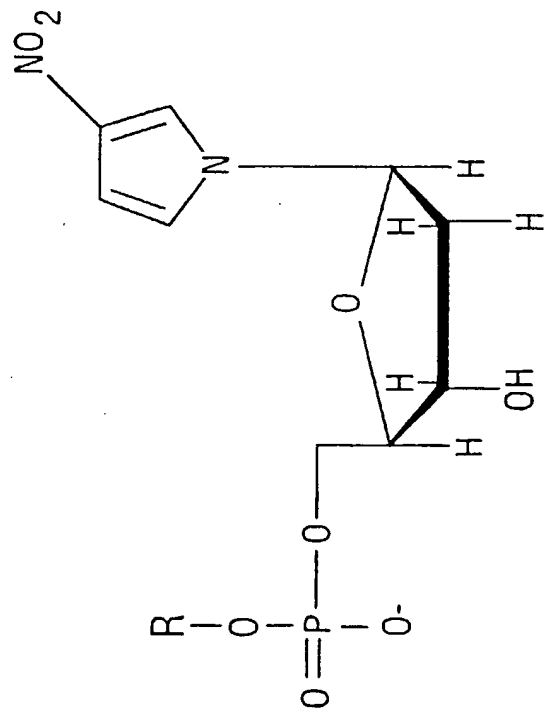
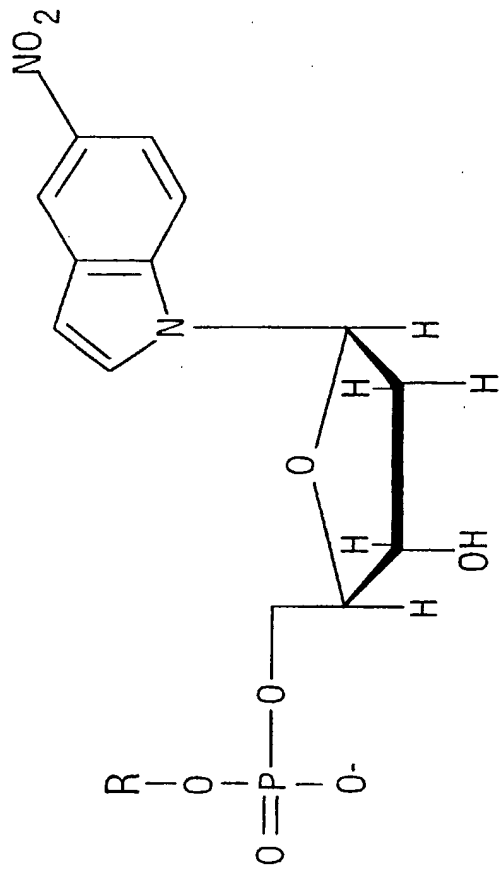


FIG. 72B



3-NITROPYRROLE



5-NITROINDOLE

FIG. 73

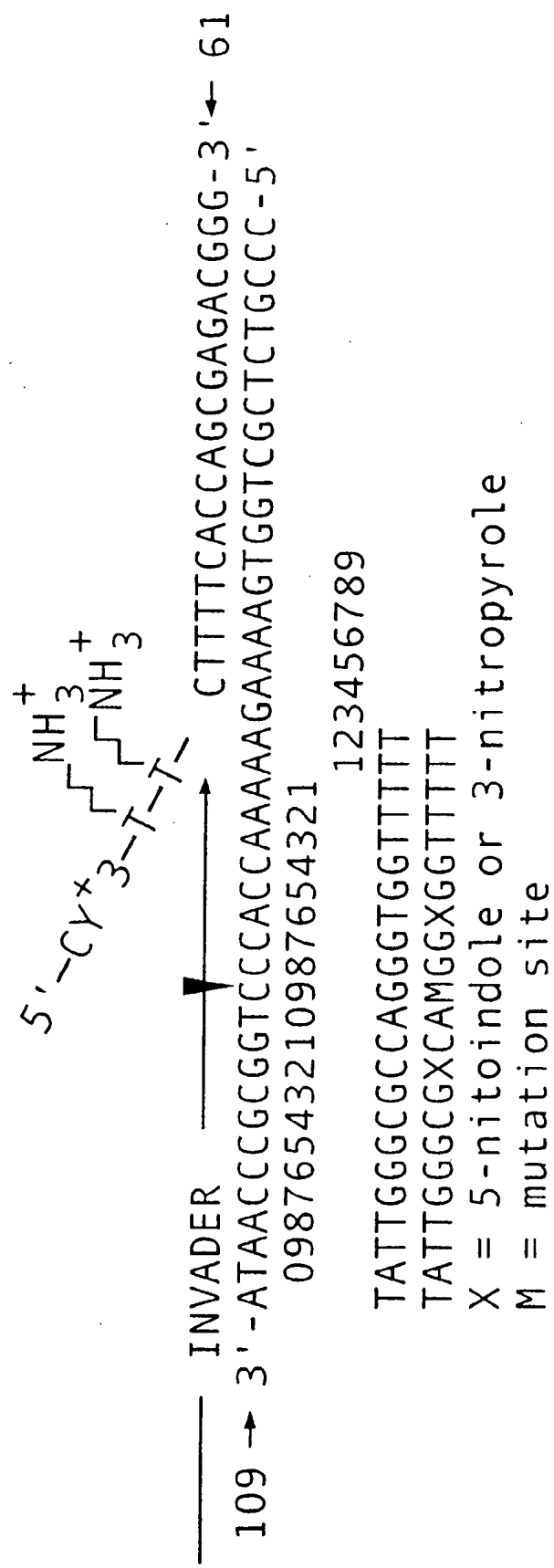


FIG. 74

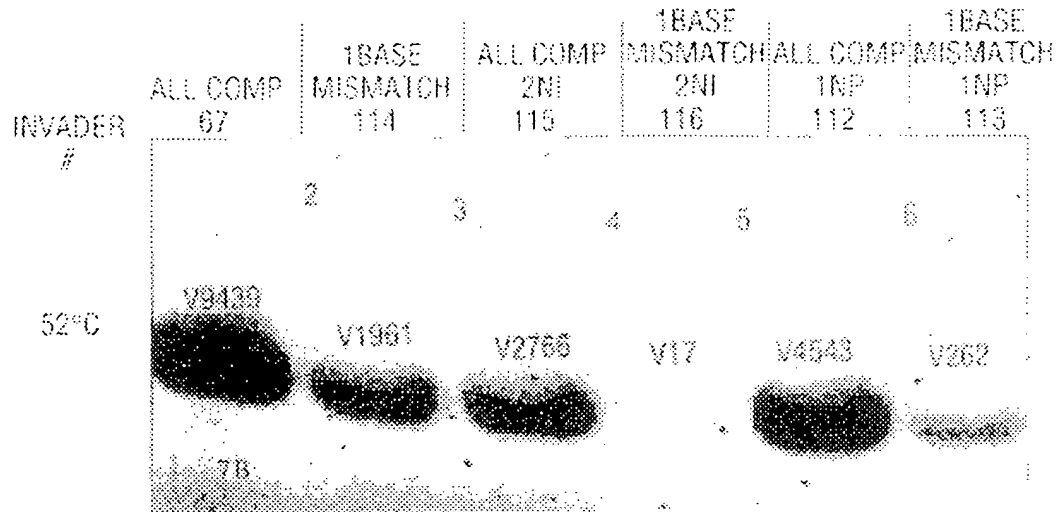


FIG. 75A

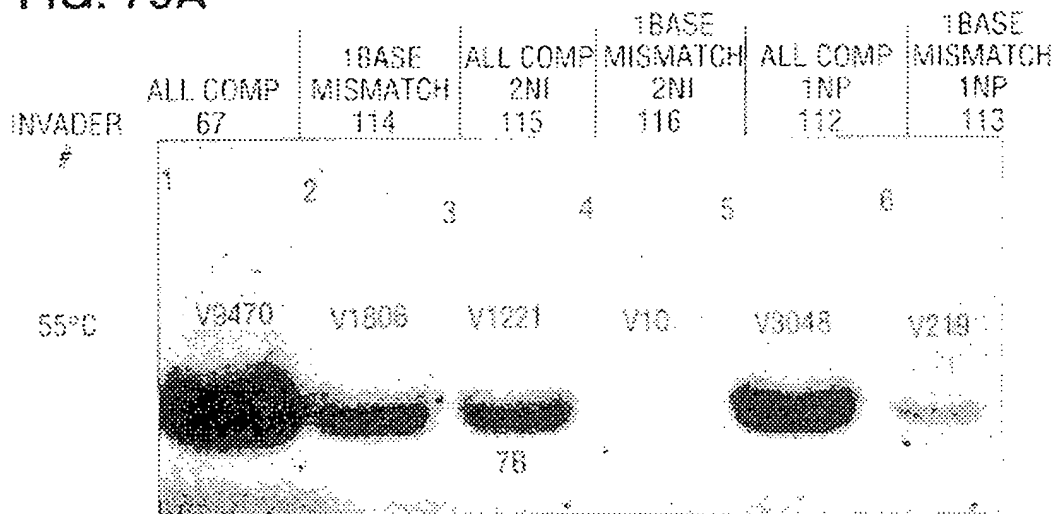


FIG. 75B

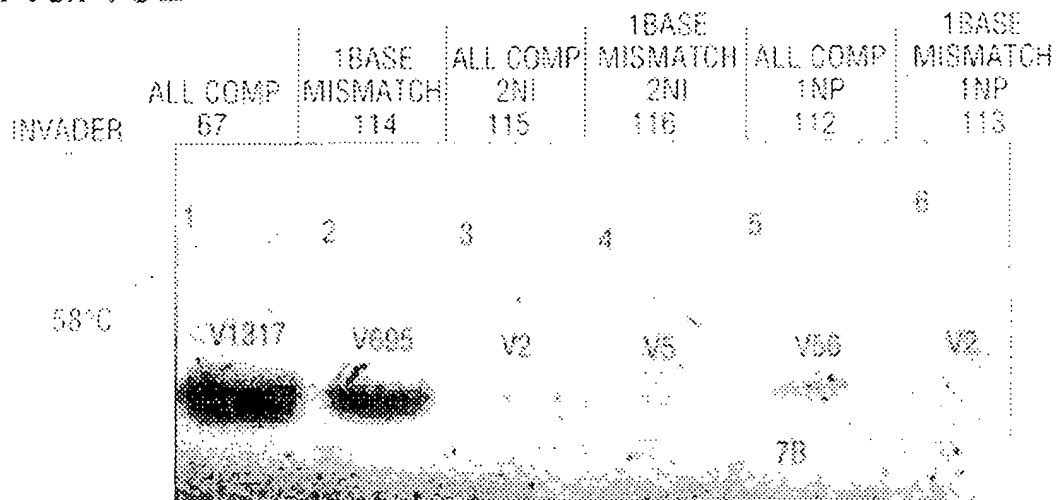


FIG. 75C

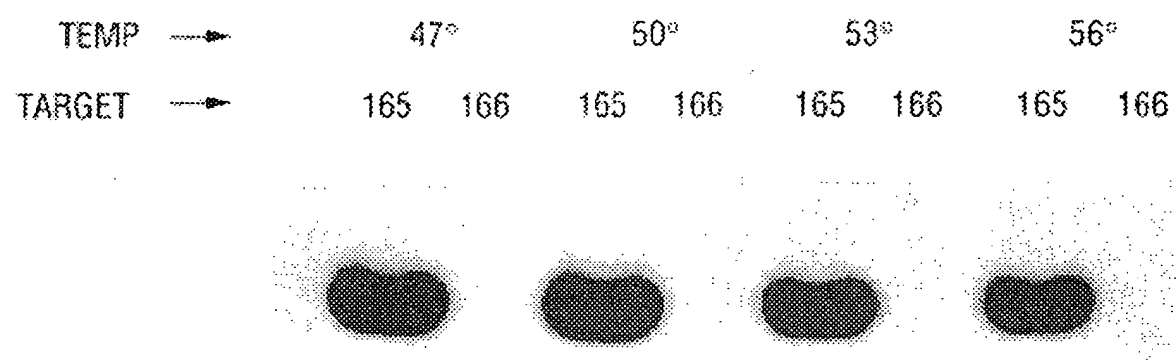


FIG. 77

F1

5' GTTCTCTGCTCTCTGGT 1819
 ↓ ↓
 CGCTGTCTCGCTTGT^G
 GCGACAGAGCGAACA^A
 3' GCTCTCTGGT

FIG. 78A

F1

5' GTTCTCTGCTCTCTGGT 2122
 ↓ ↓
 CGCT GTCTCGCTTGT^G
 3' GCTCTCTGGTGCGACAGAGCGAACA^A
 5' CGAGAGACCACGCT^G
 P15

FIG. 78B

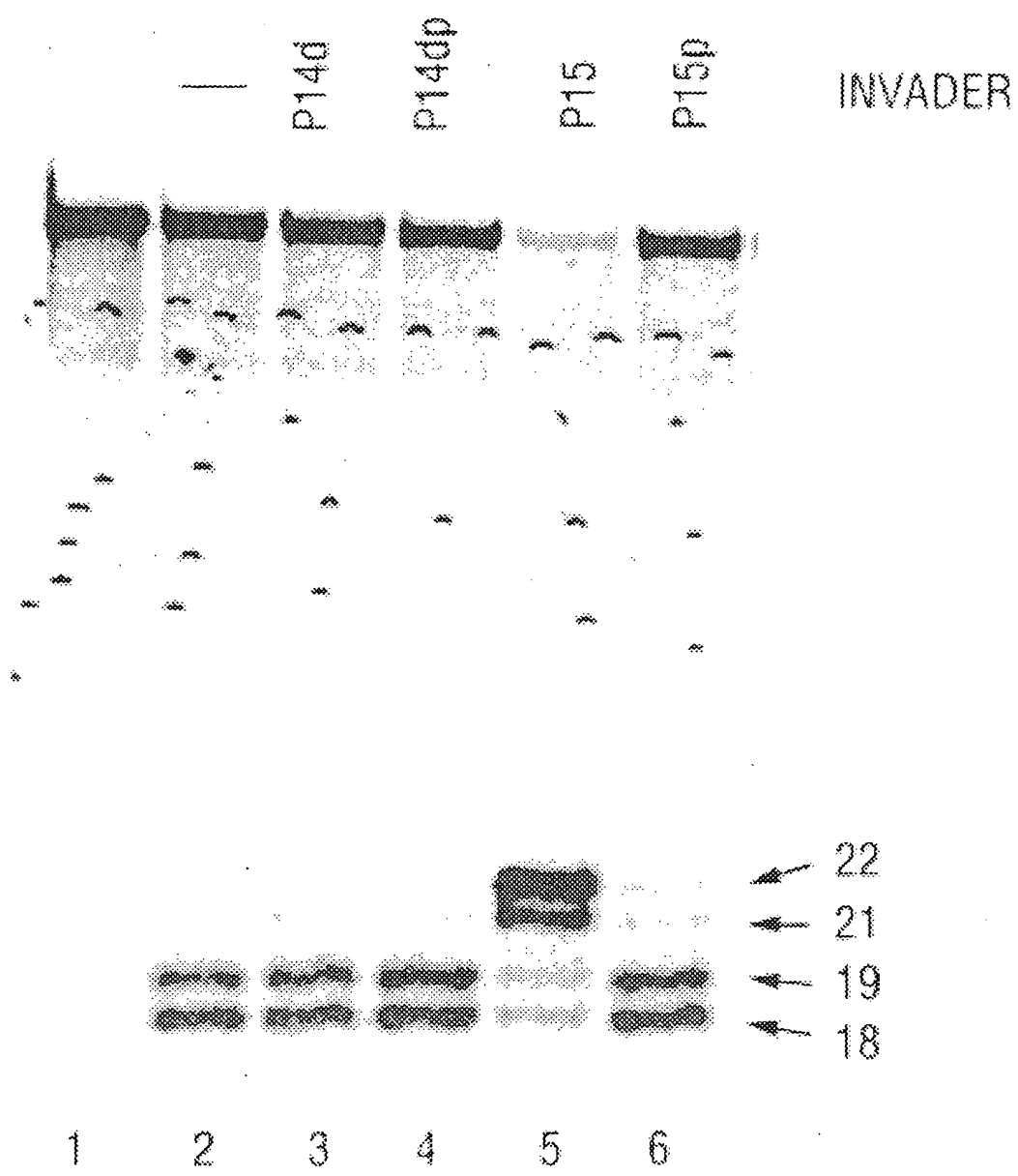


FIG. 78C

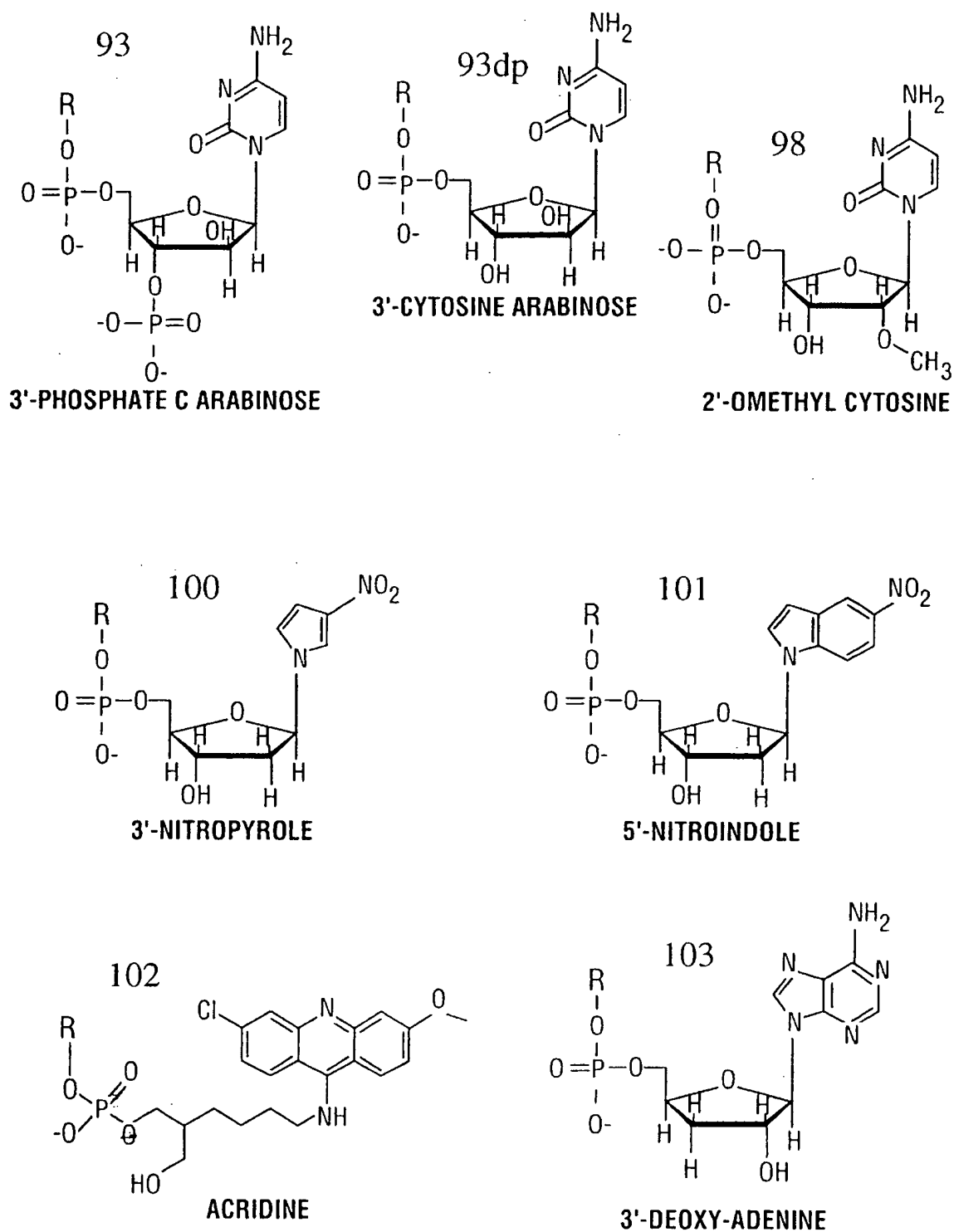
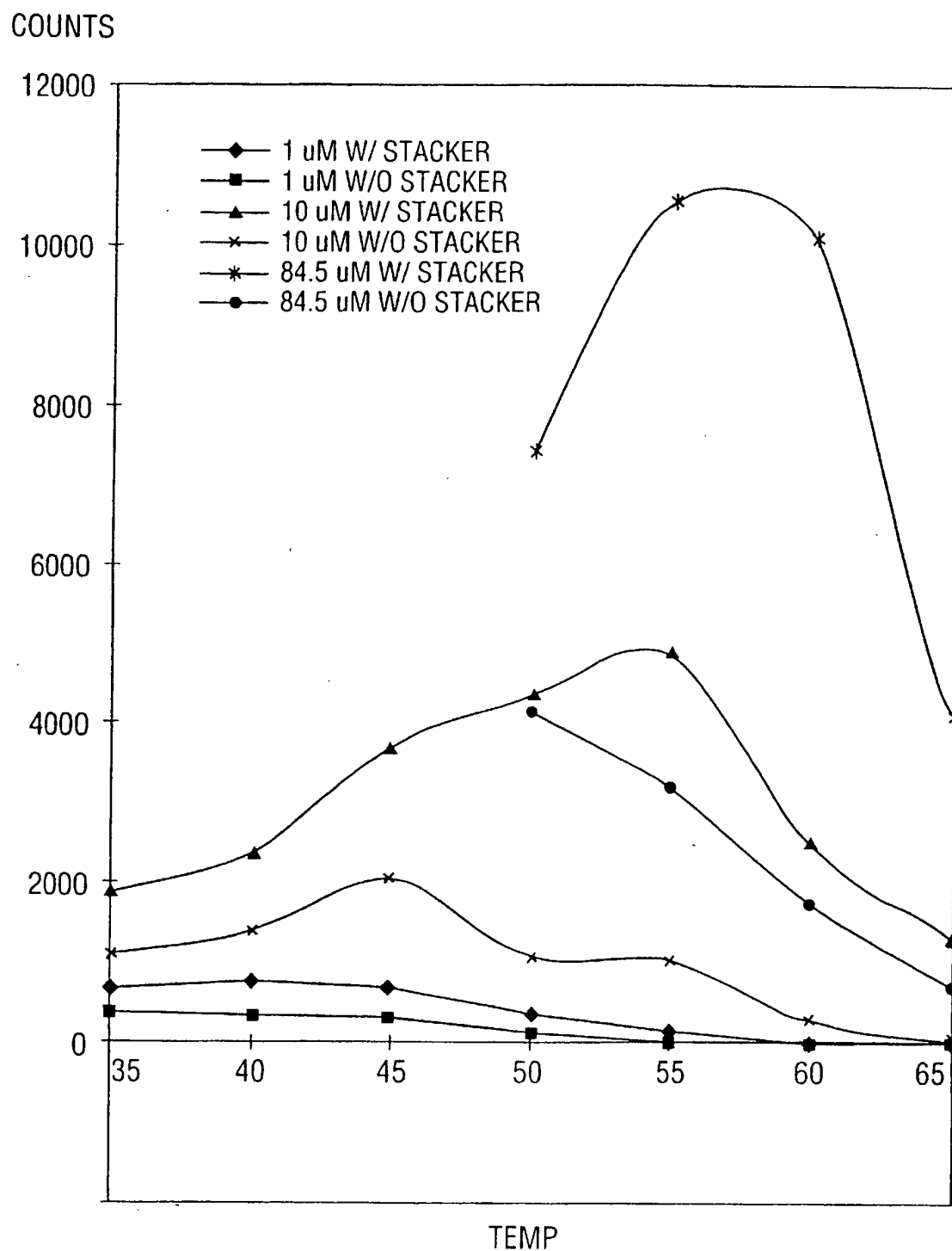


FIG. 79



CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIG. 80

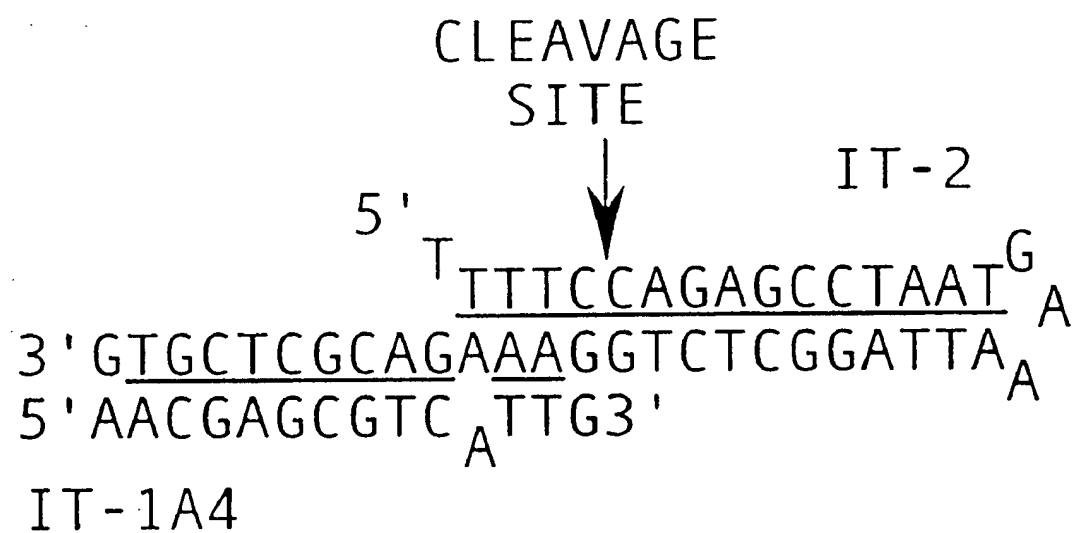
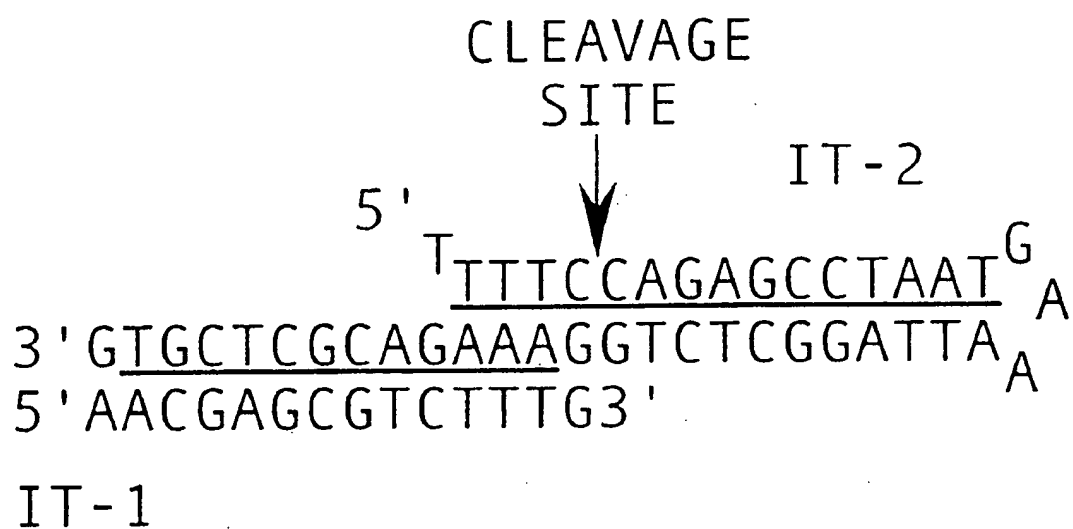


FIG. 81

1 2 3 4



— UNCUT



FIG. 82

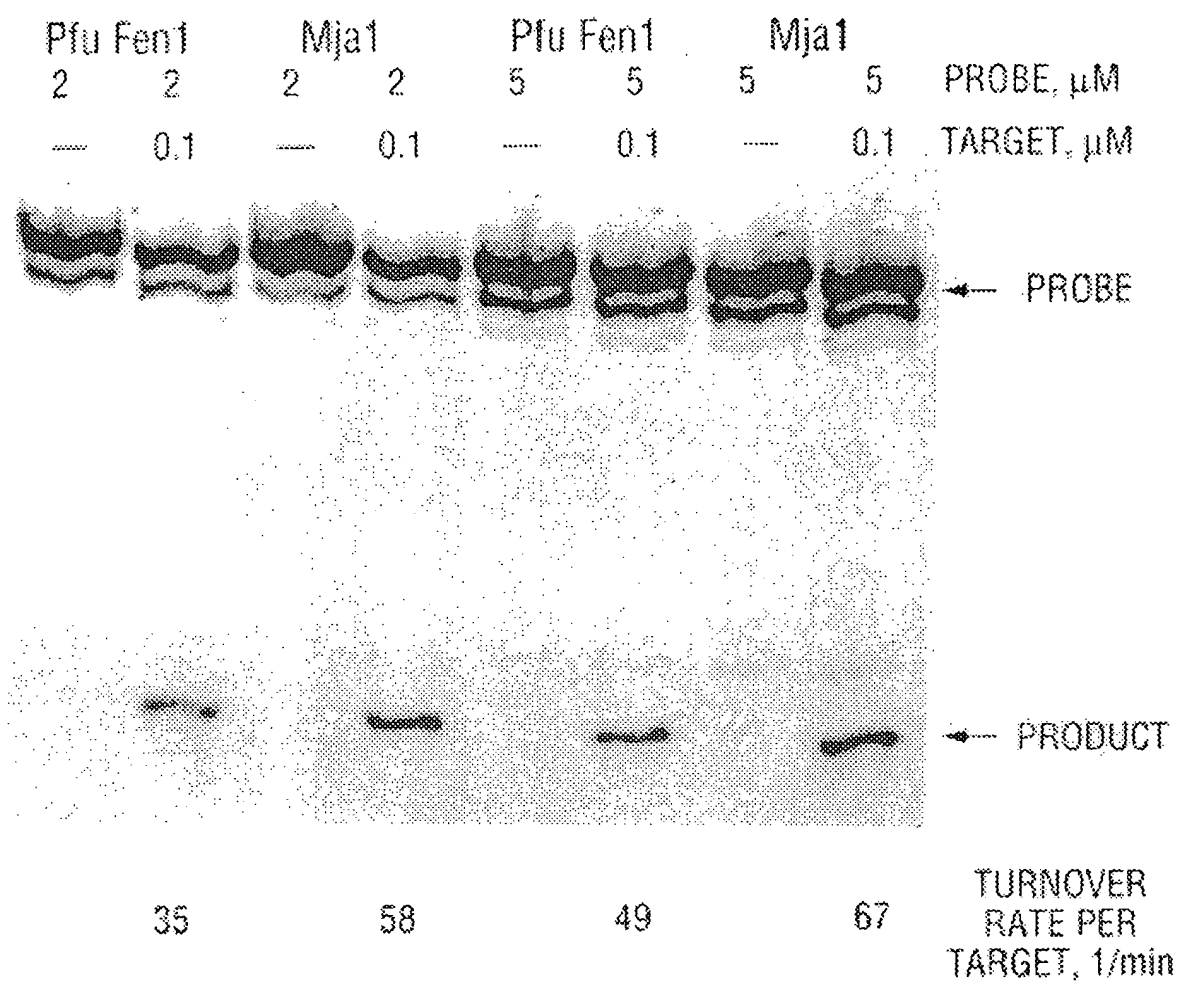


FIG. 83

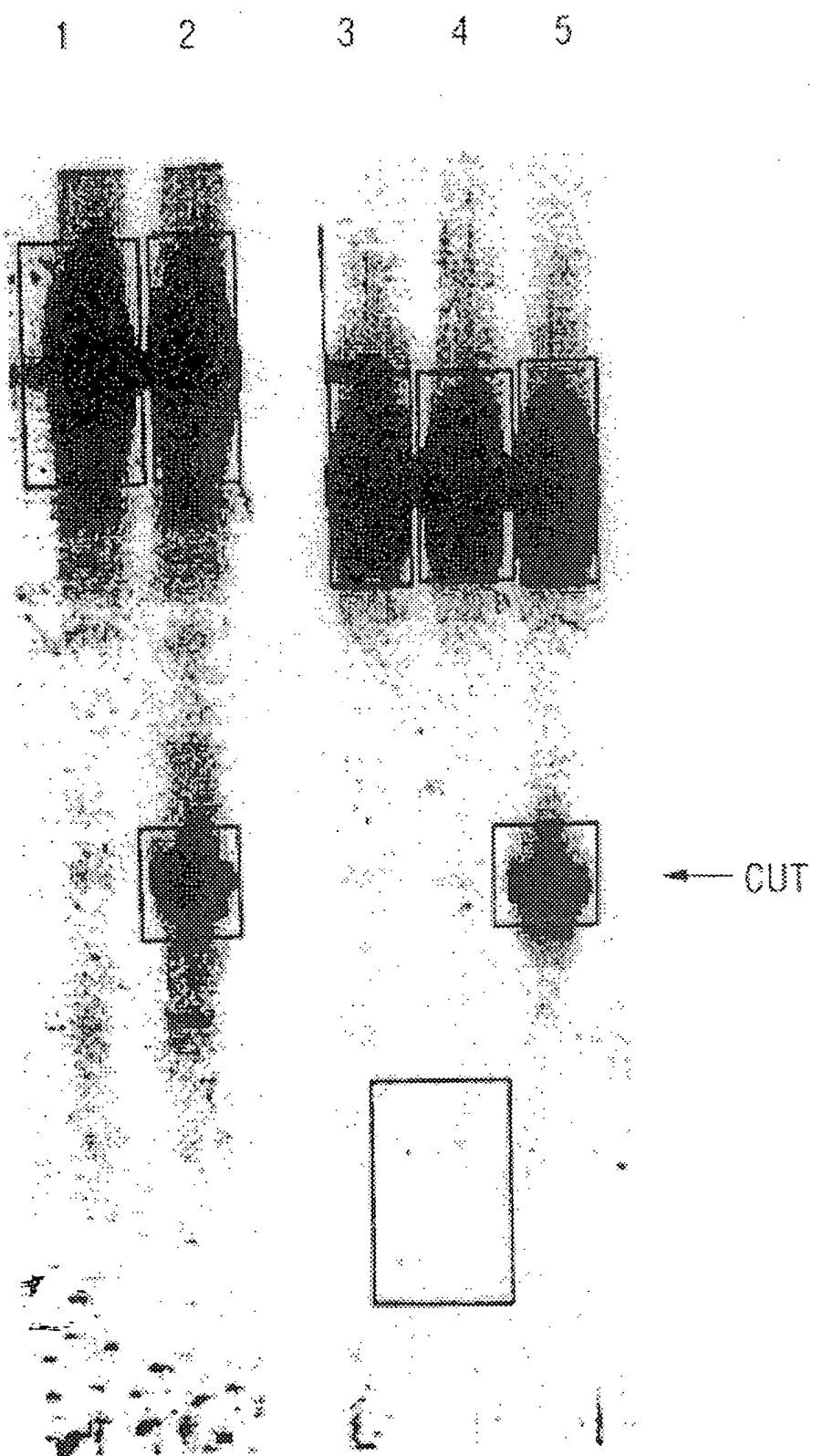
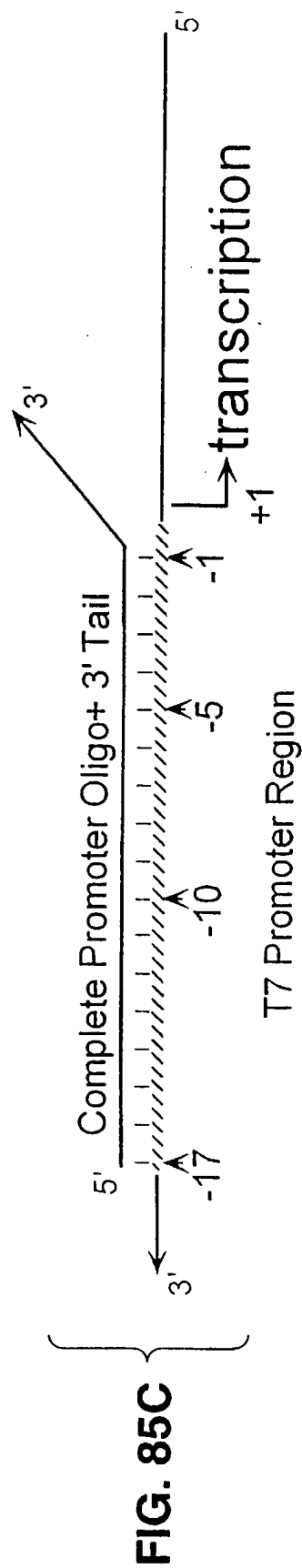
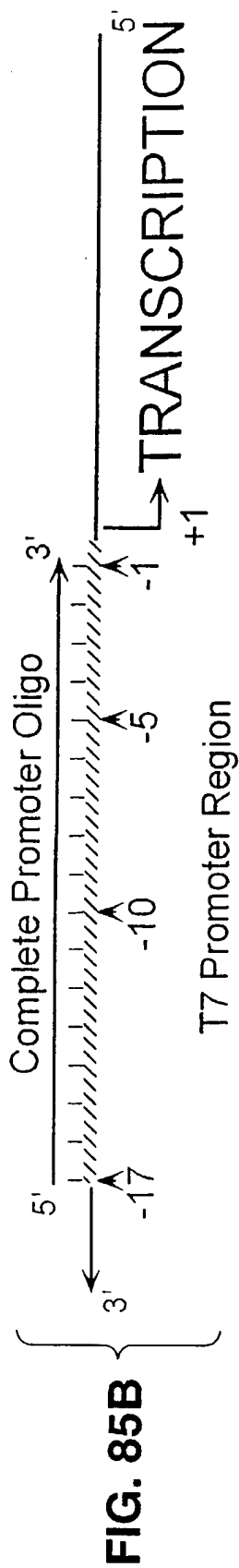
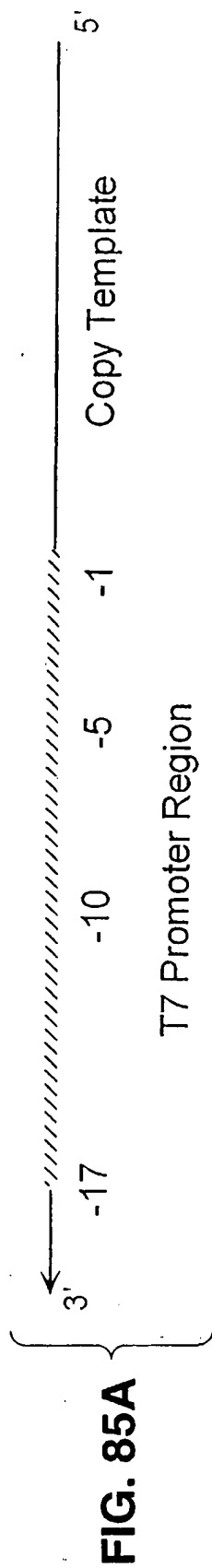
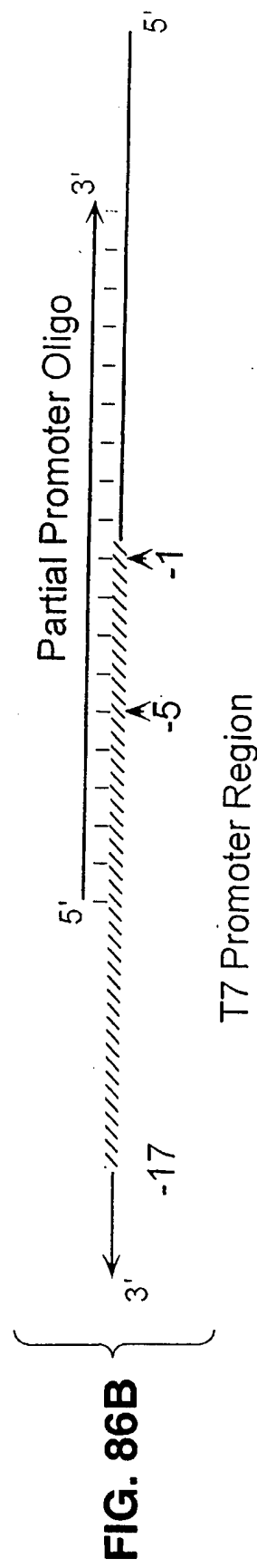
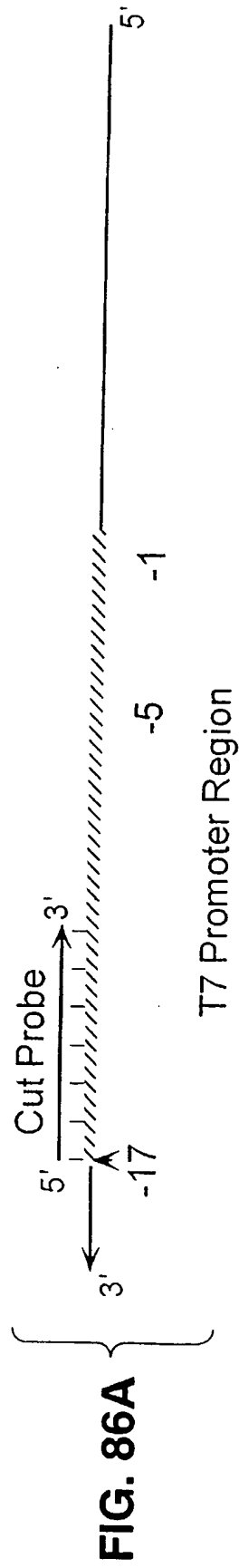


FIG. 84





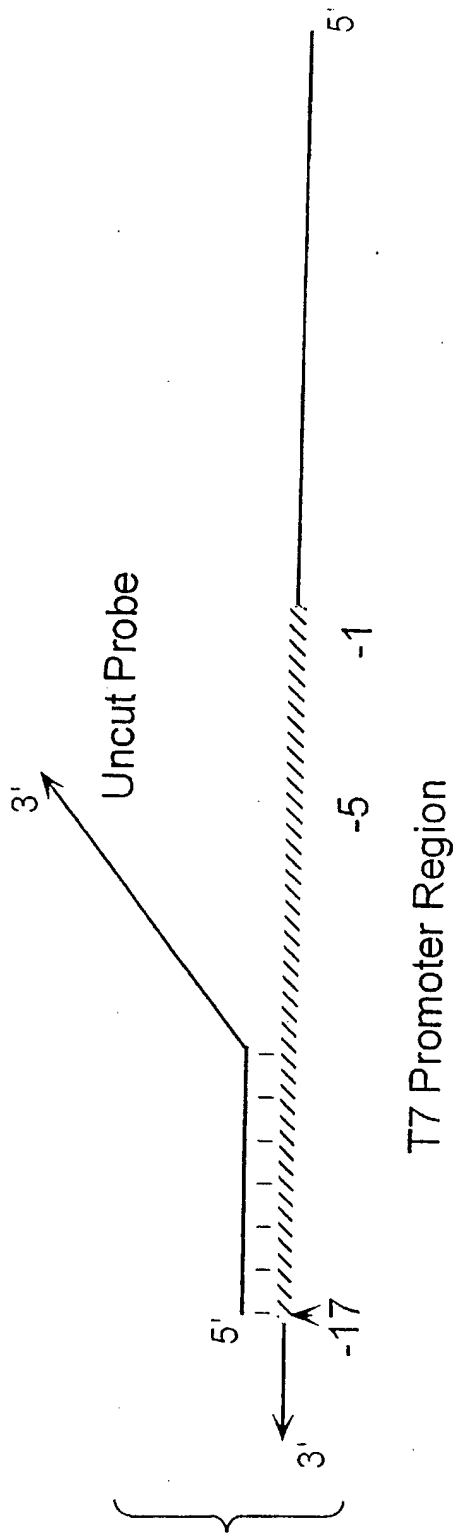


FIG. 86C

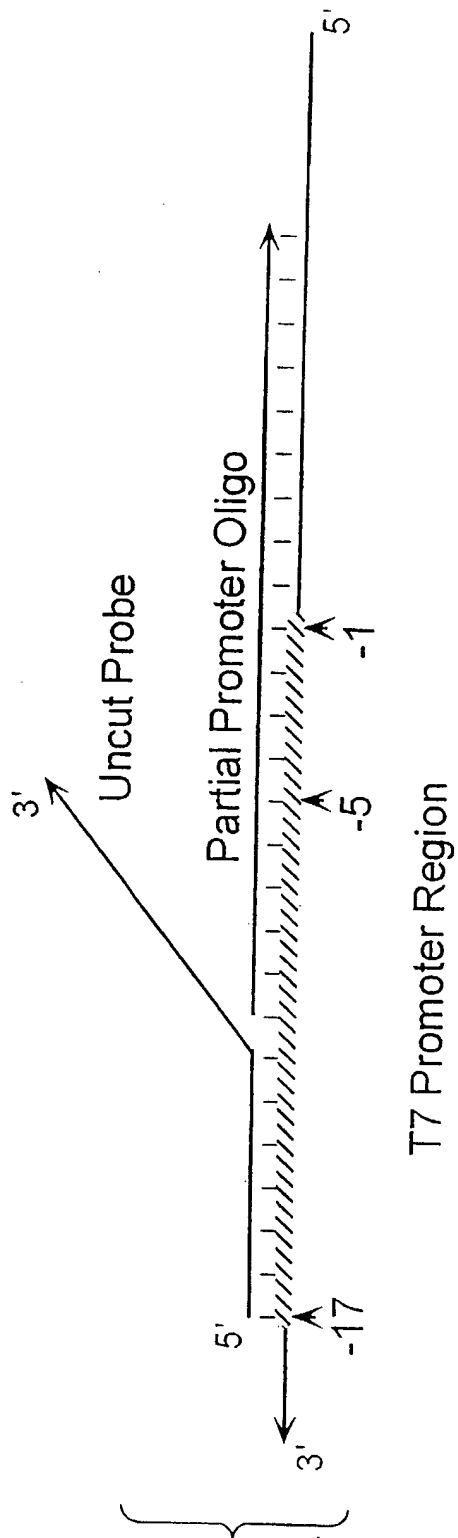


FIG. 86D

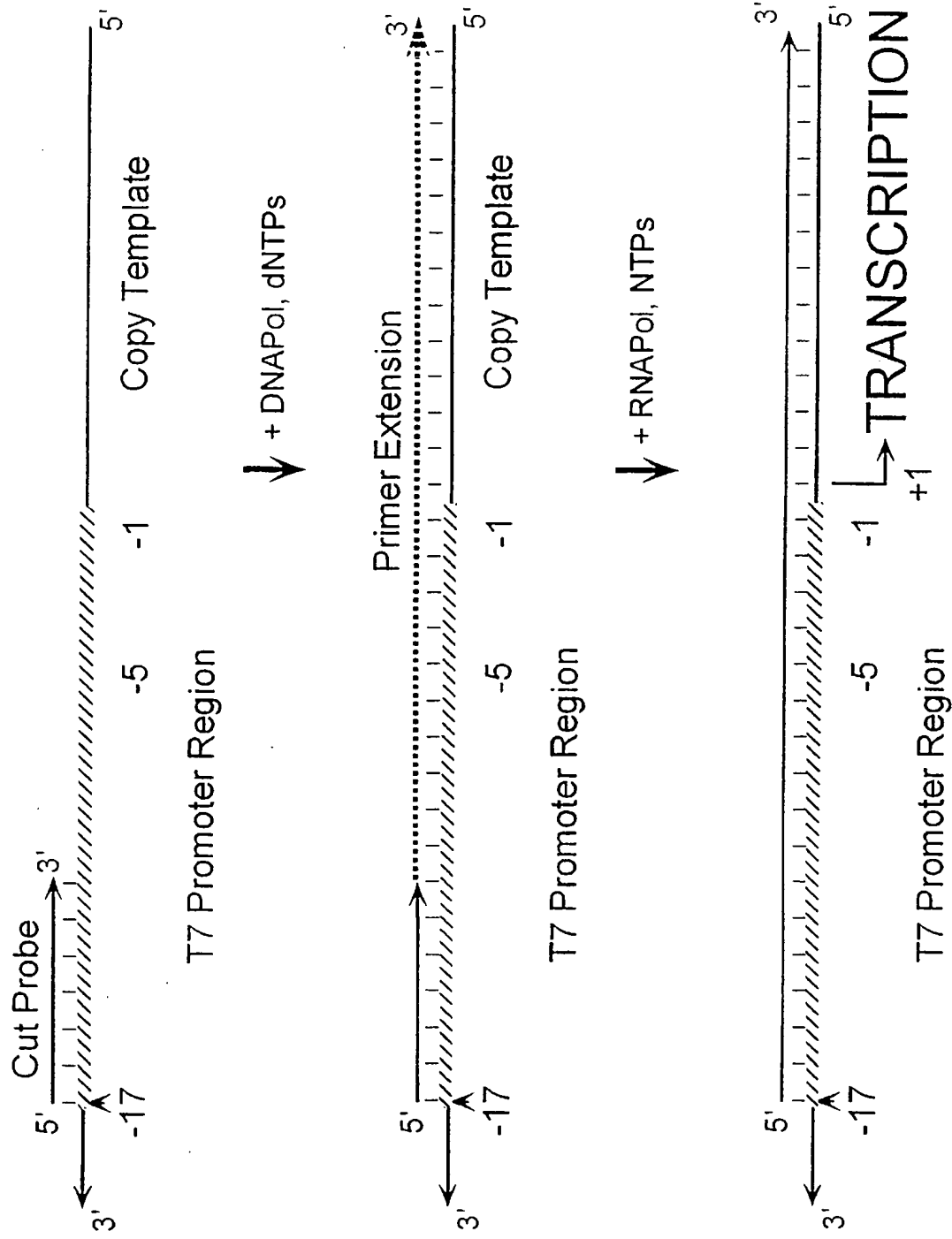
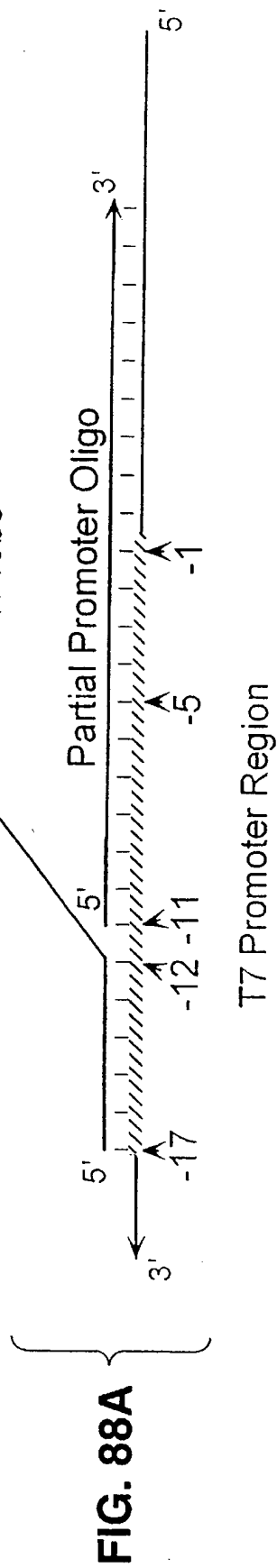


FIG. 87



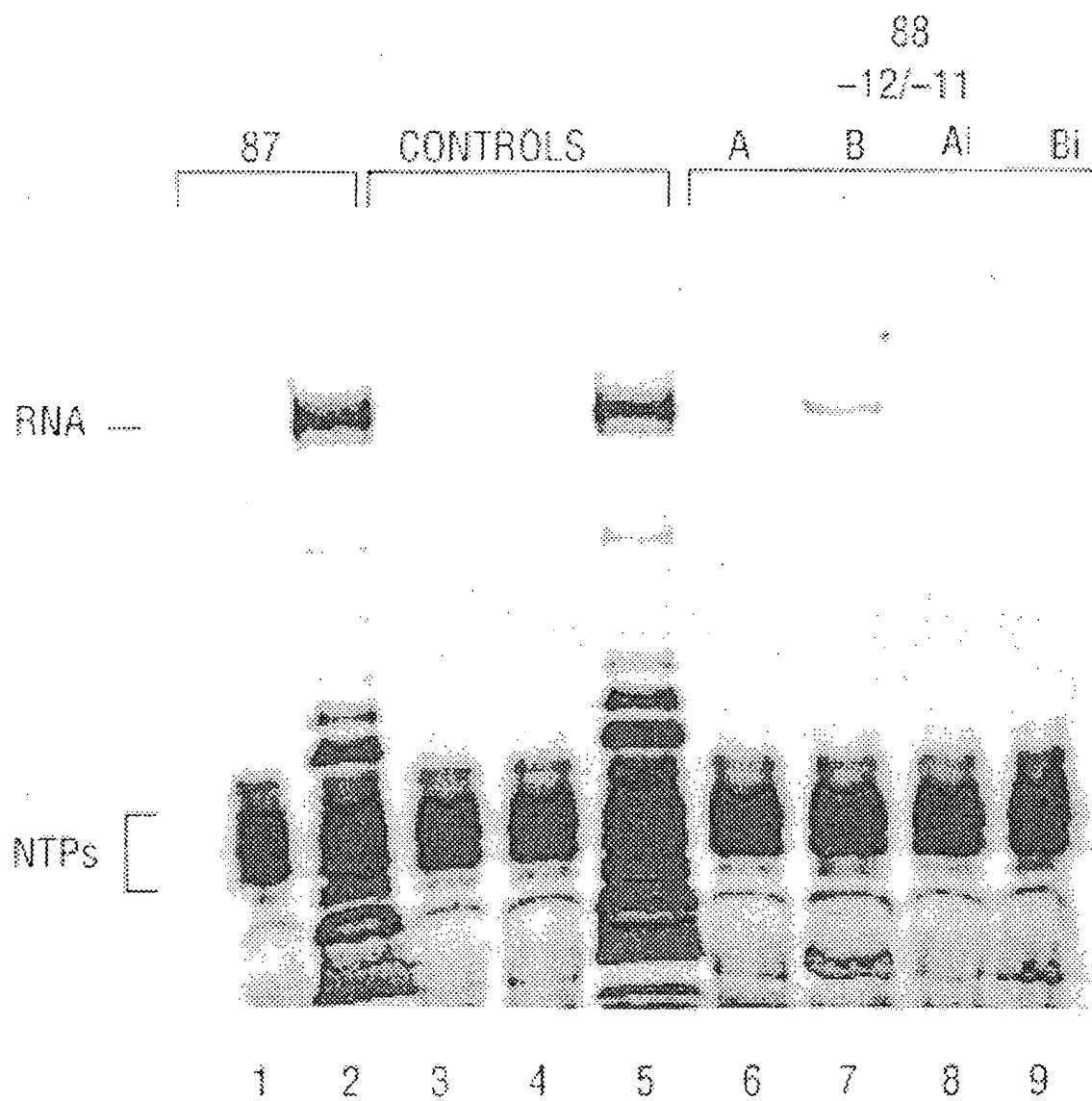
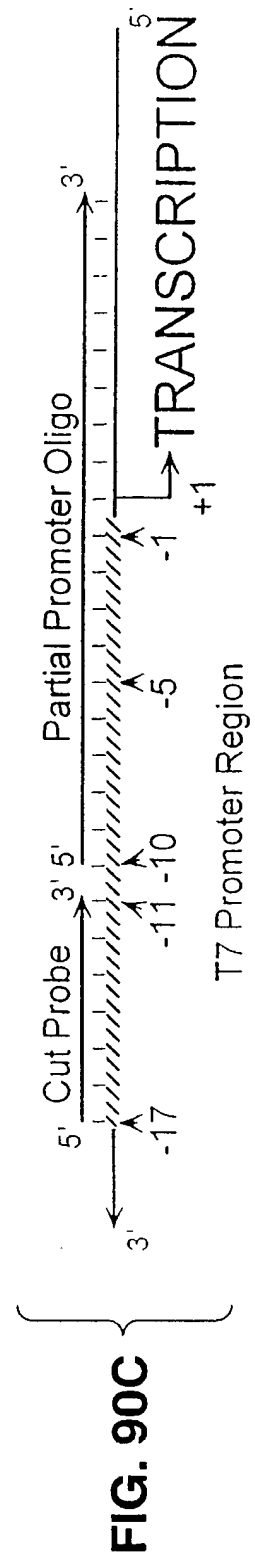
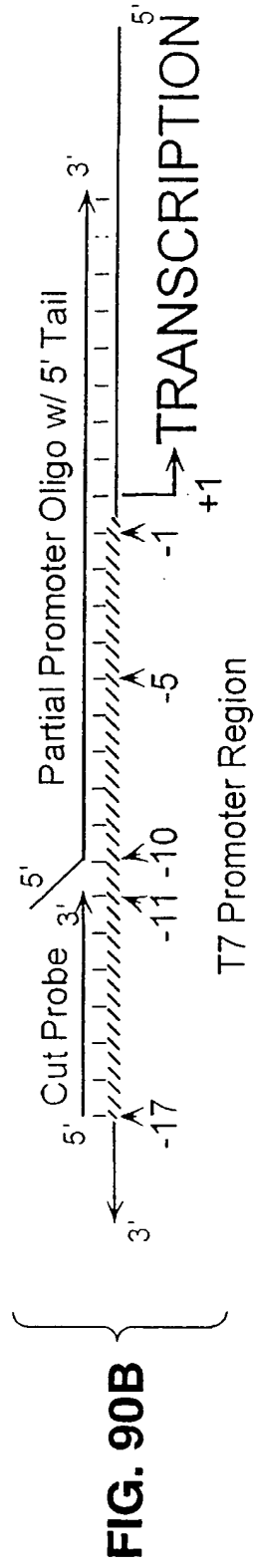
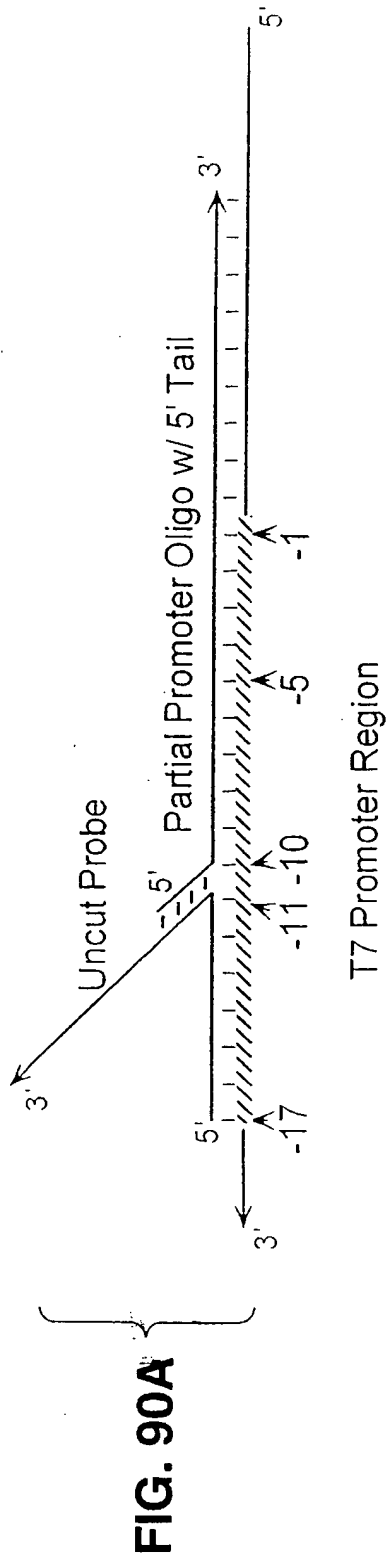


FIG. 89



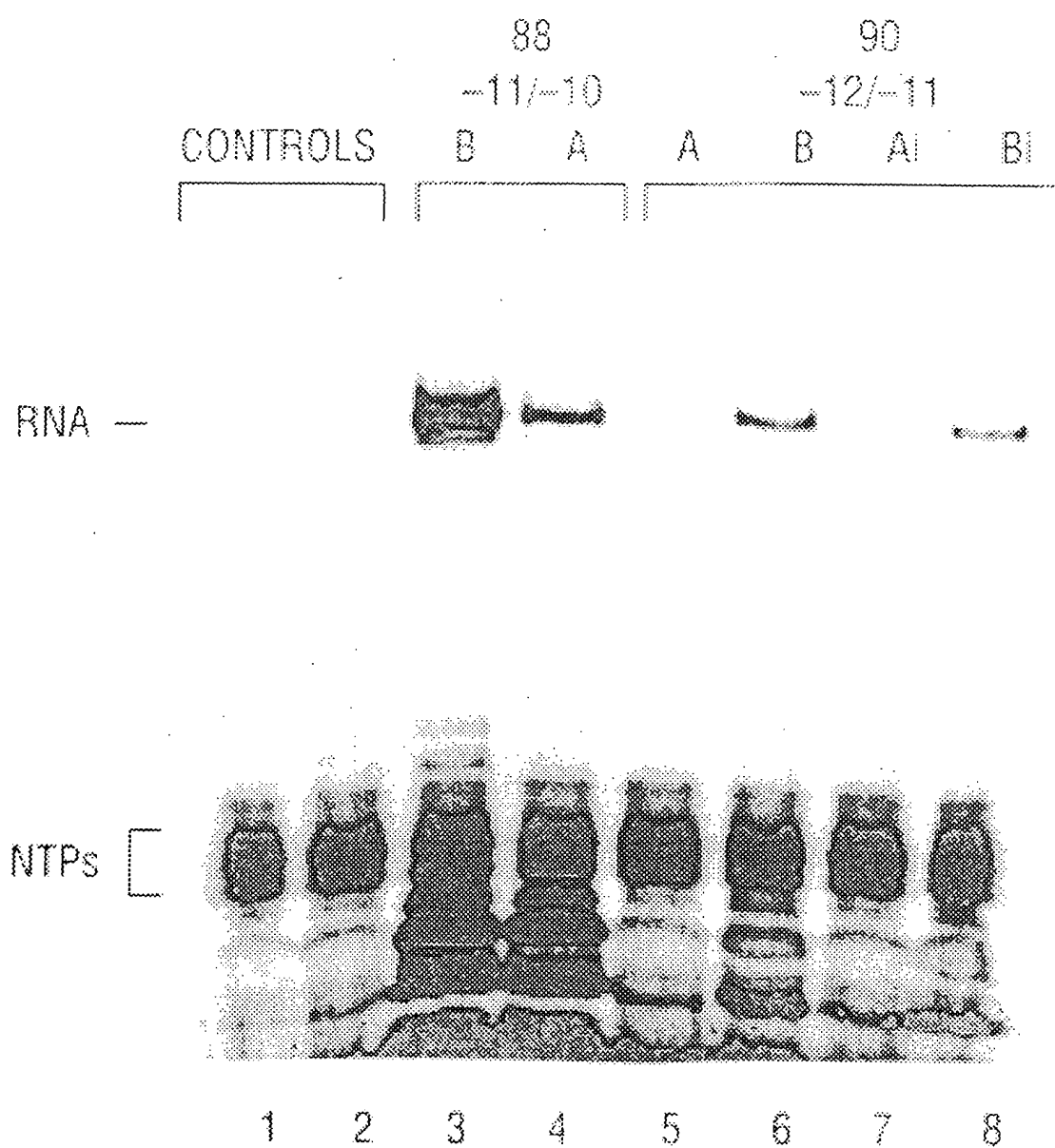


FIG. 91

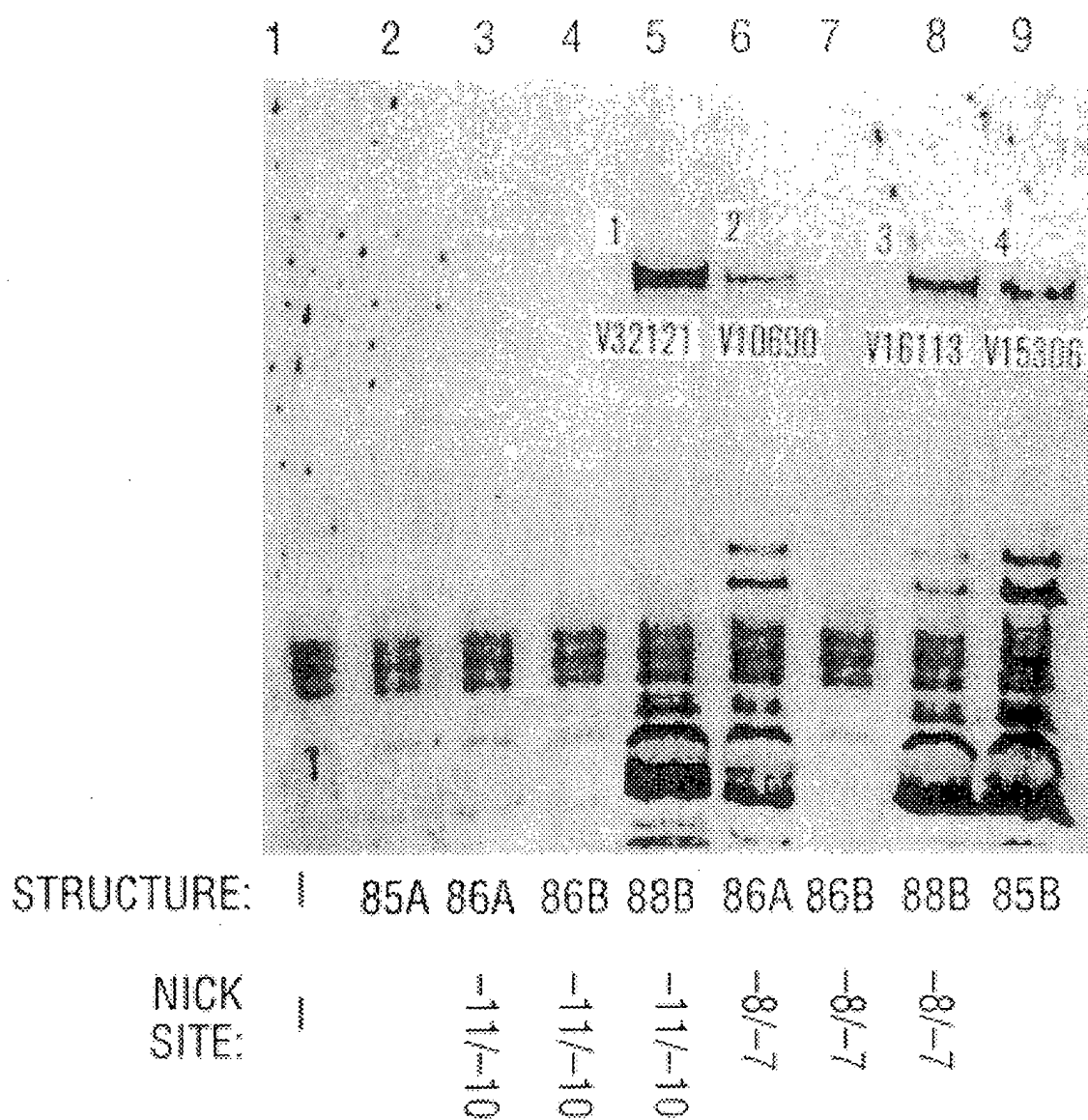


FIG. 92

1 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93A

2 5'-cgaaattaatacgactcactata-3'
 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93B

#073-065
 5'-cgaaattaatacgactcactataccagaa-3'
 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93C

4 NO DNA

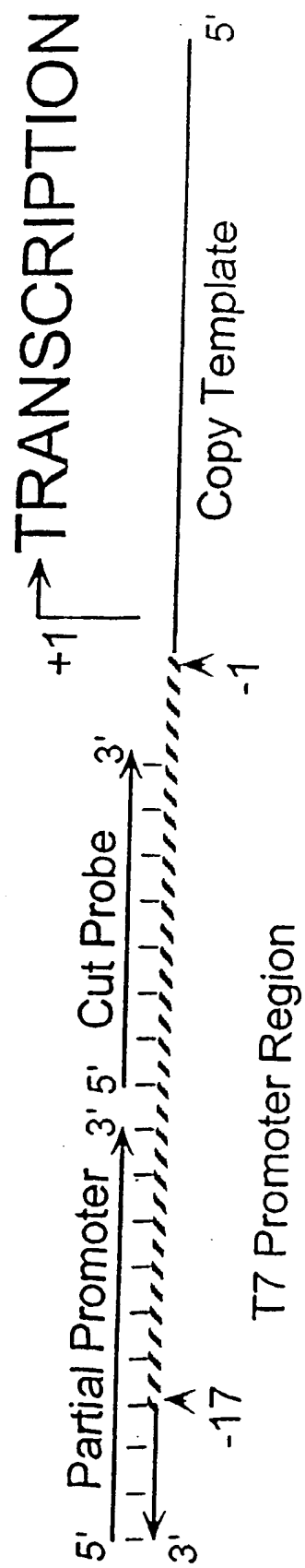
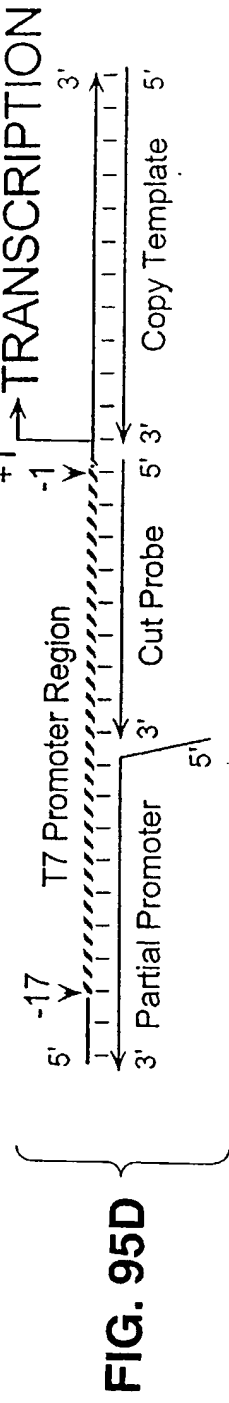
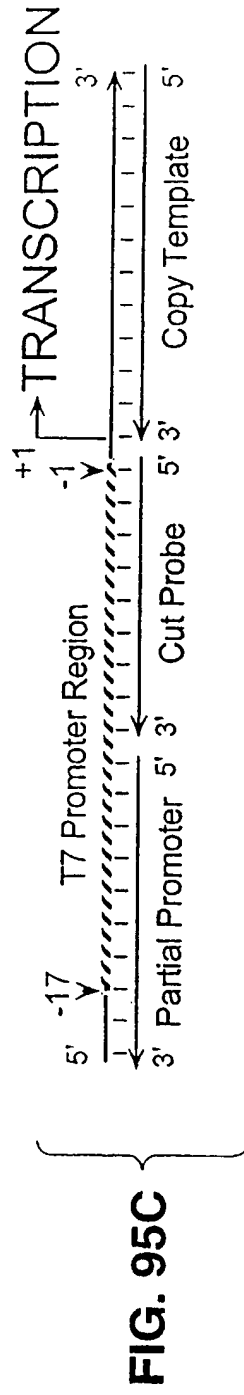
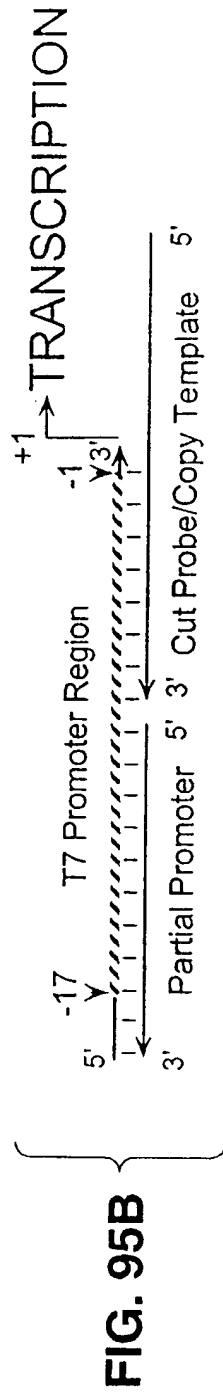
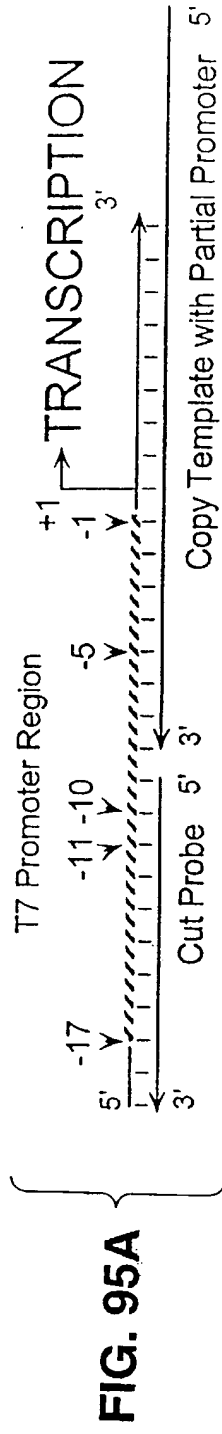


FIG. 94



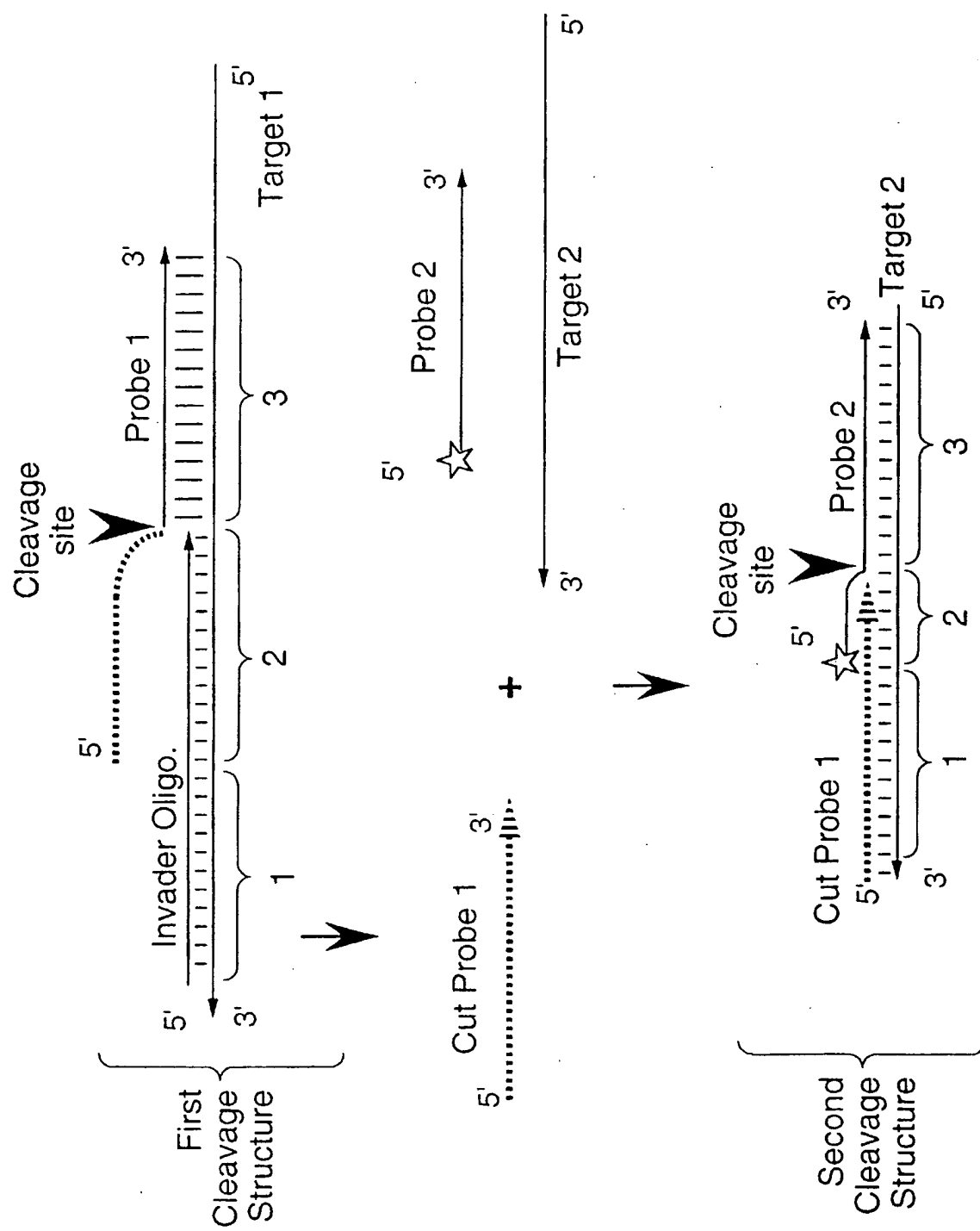


FIG. 96

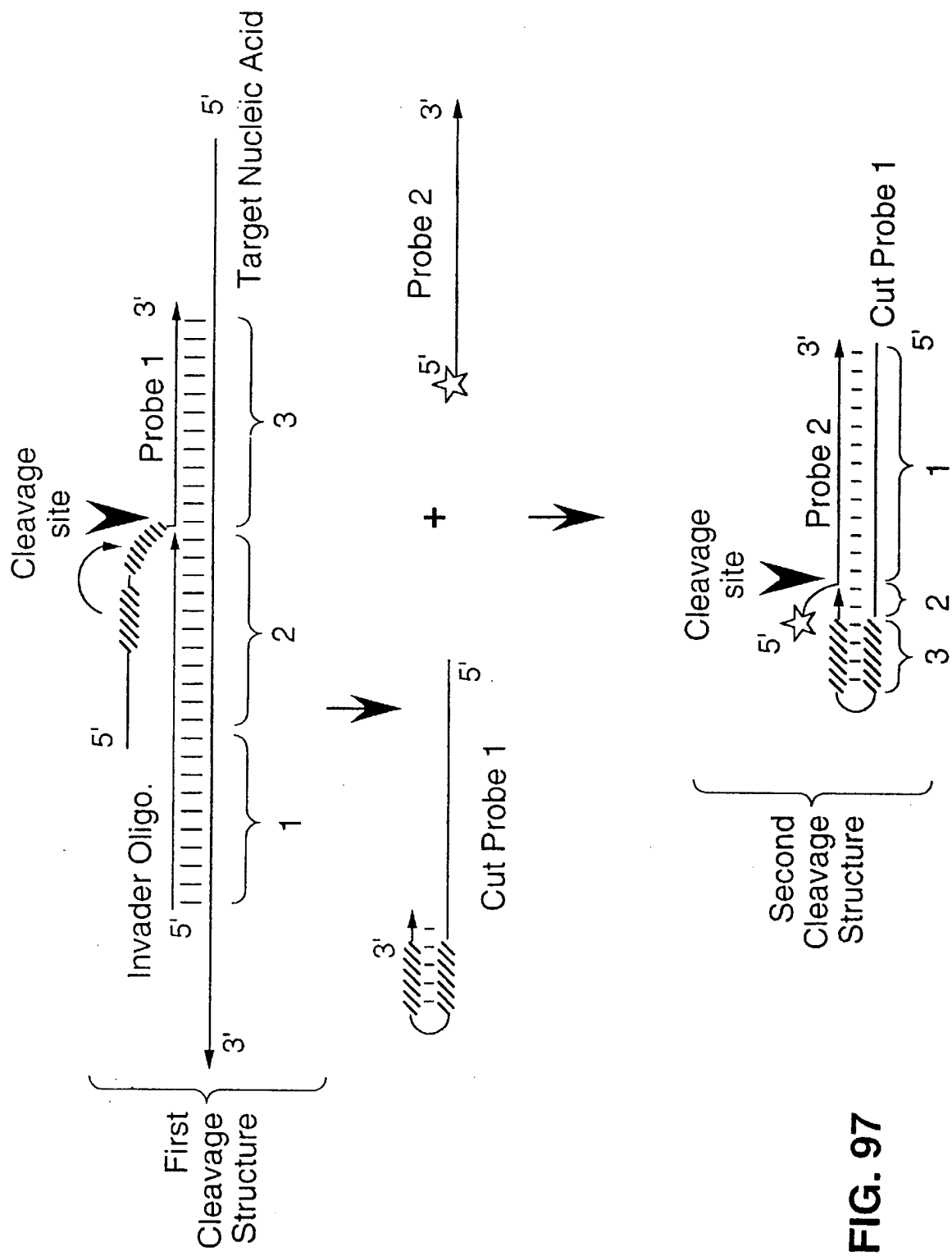


FIG. 97

PR1 probe

Cleavage site

5'FITT^TTCCAGAGCCTAAT^G3'

IT3 Invader-Target

A^AACGAGCGTCTTT^G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A^AAGCGTCTT^G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A^ACGTCTT^G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A^ATCTT^G3'
G AGAAGGTCTCGGATTAATTTTTTTTT5'

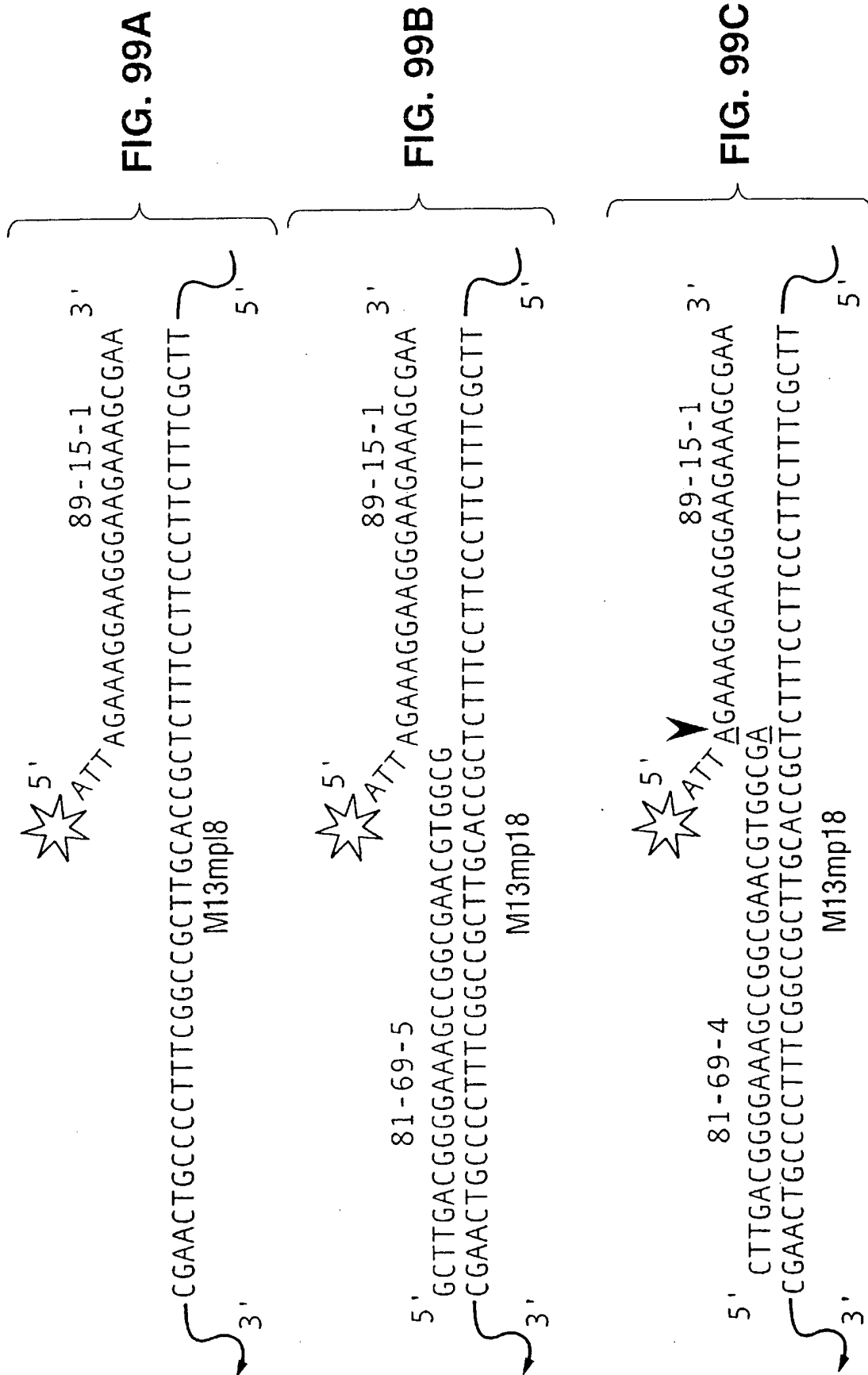
IT3-3 Invader-Target

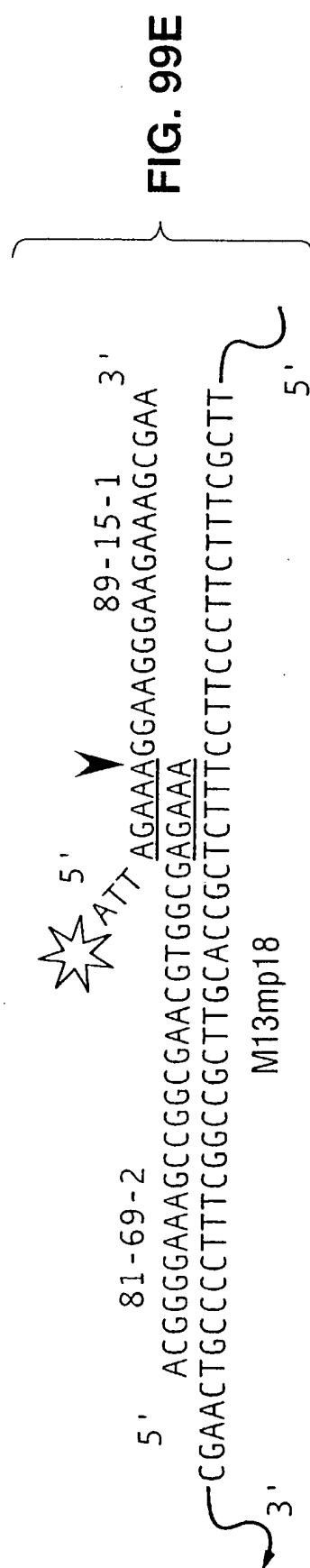
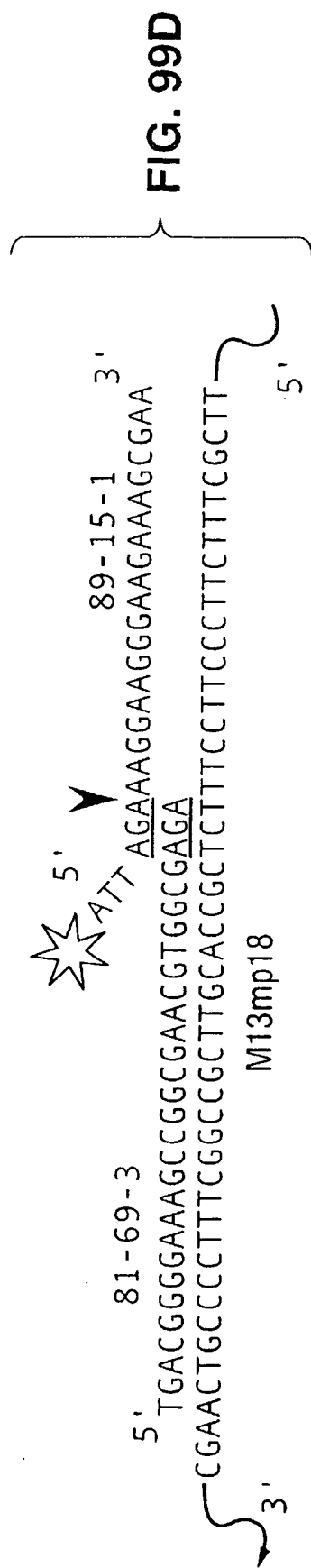
A^ACTT^G3'
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

FIG. 98





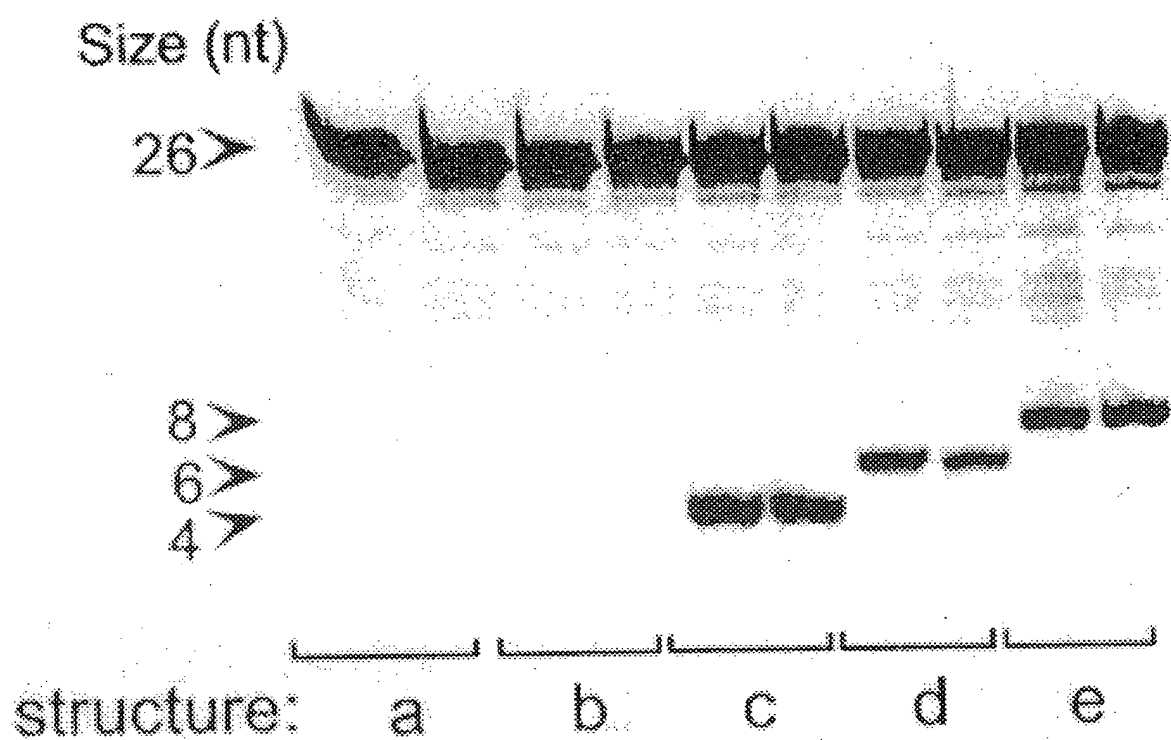


FIG. 100

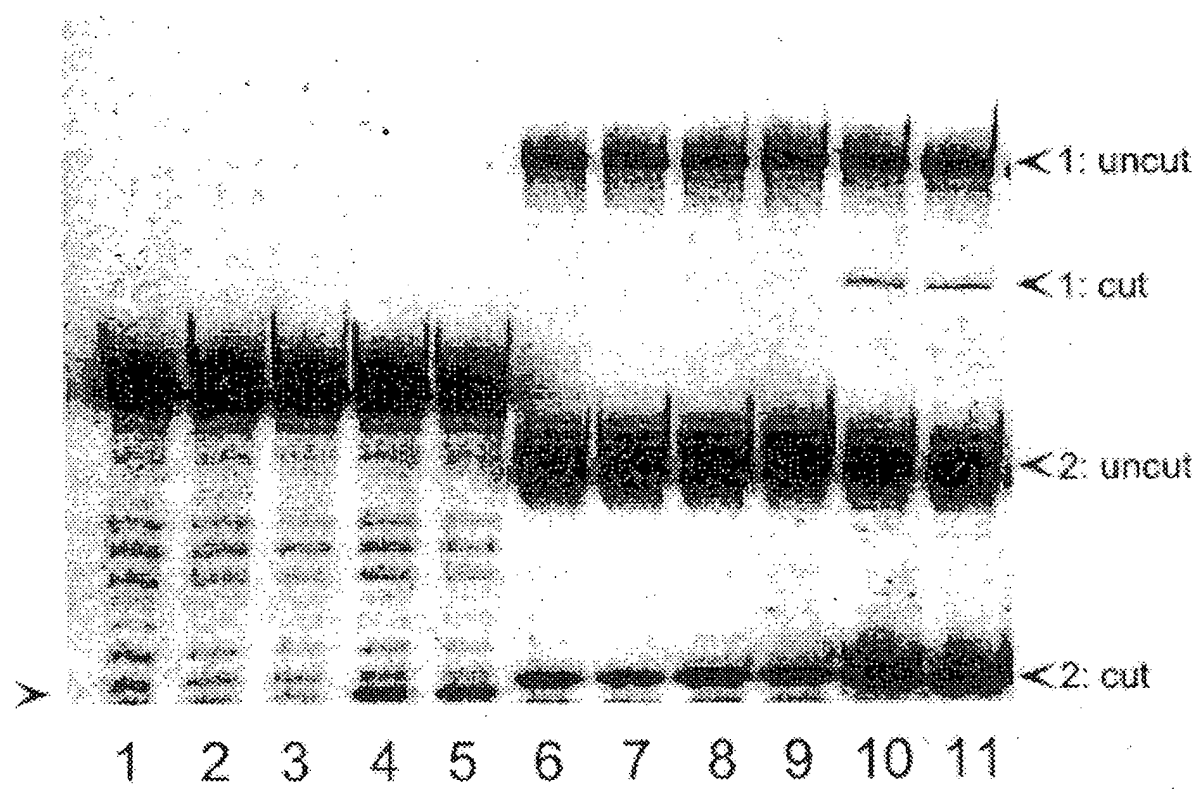
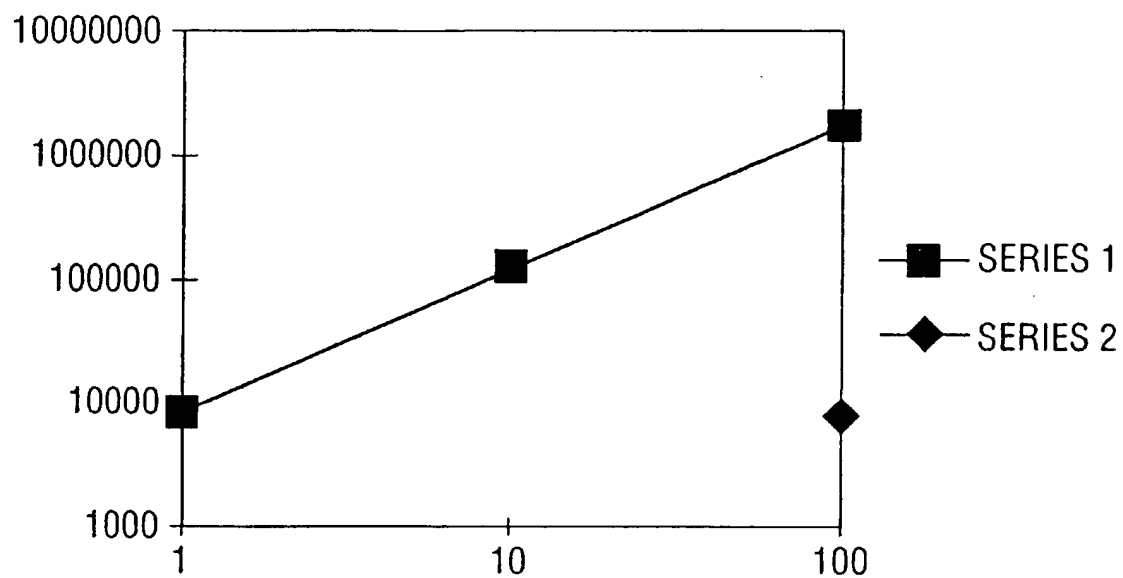


FIG. 101A



attomoles/target	basic invader	invader sqrd
1		8386
10		133185
100	8512	1862211

FIG. 101B

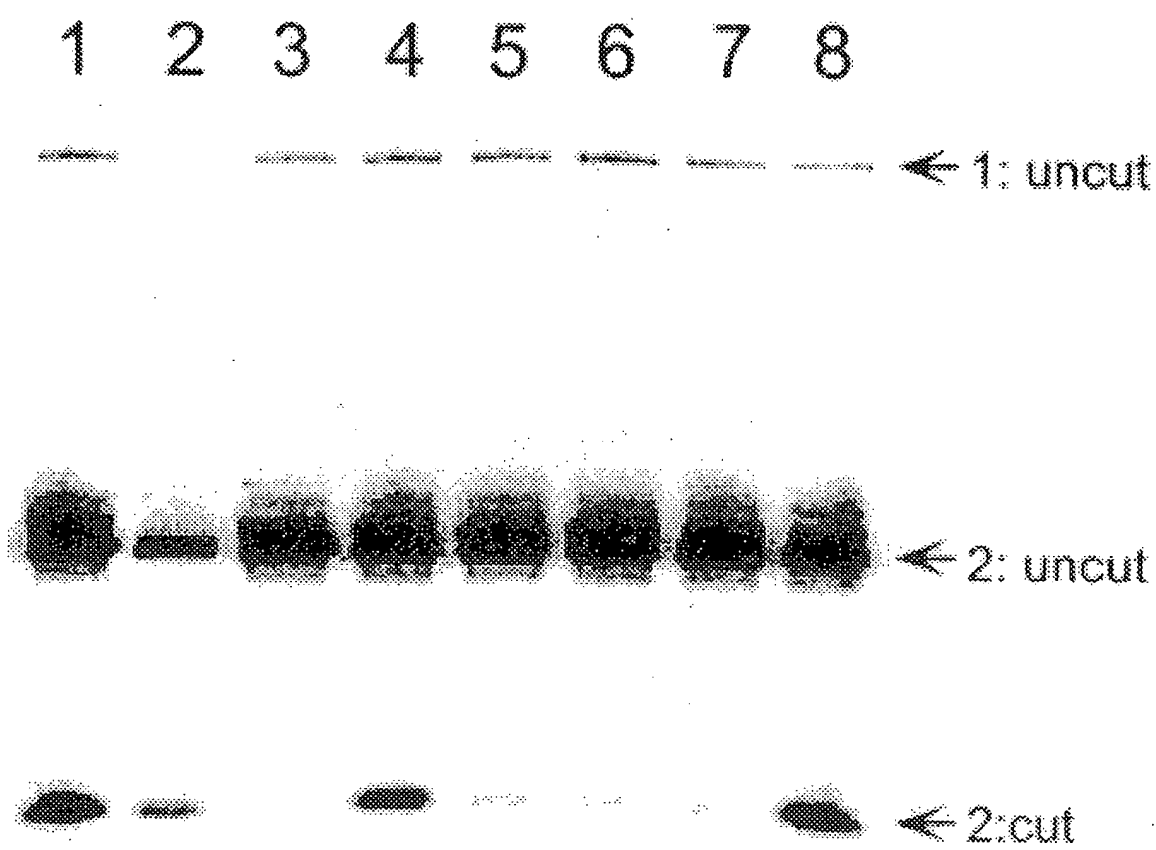


FIG. 102

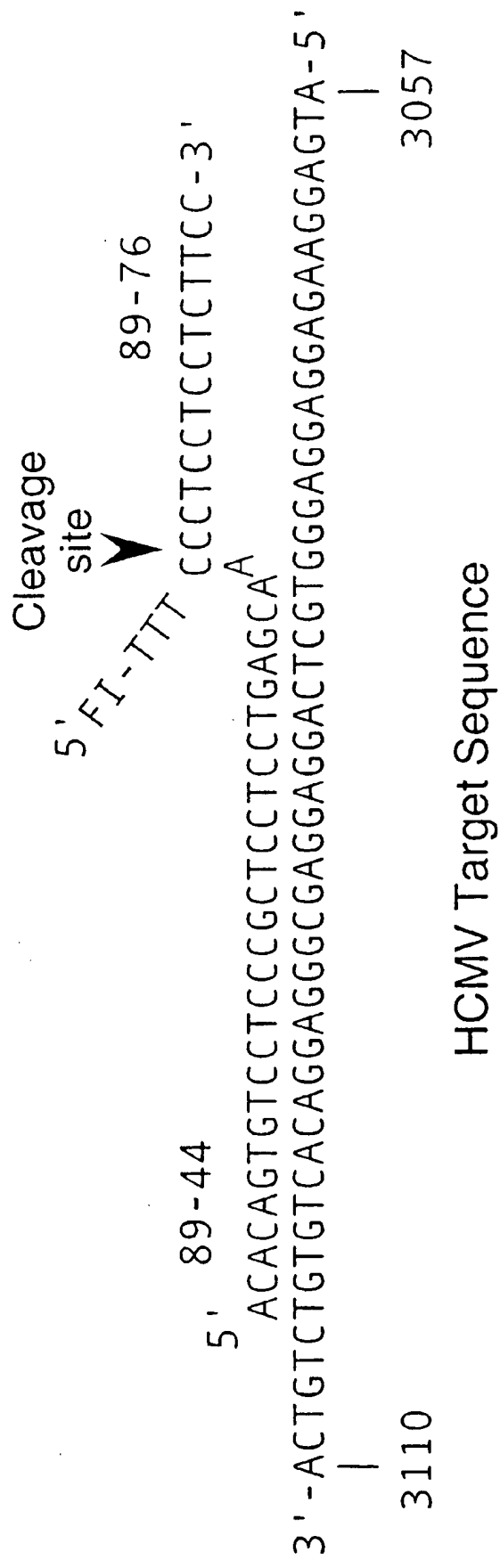


FIG. 103

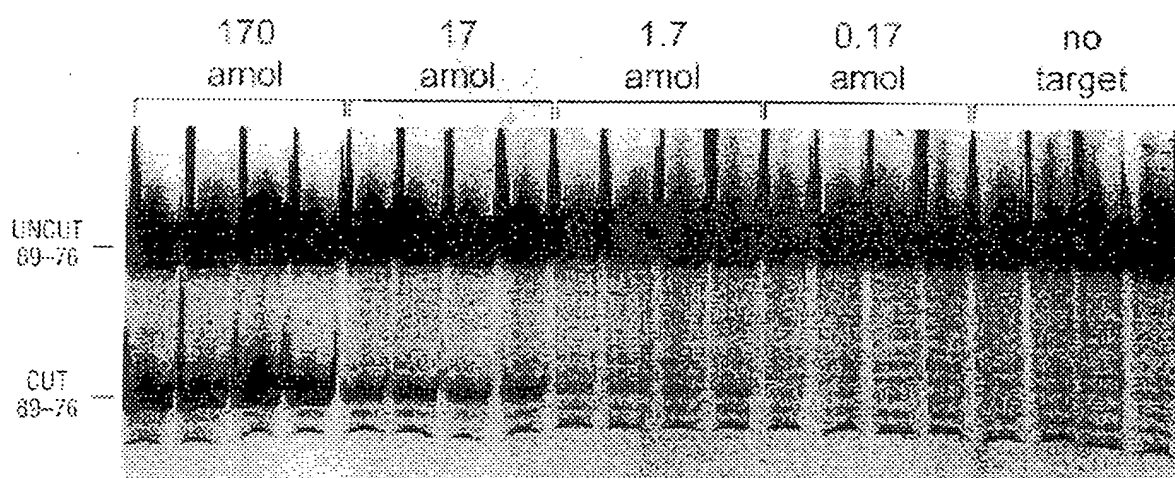
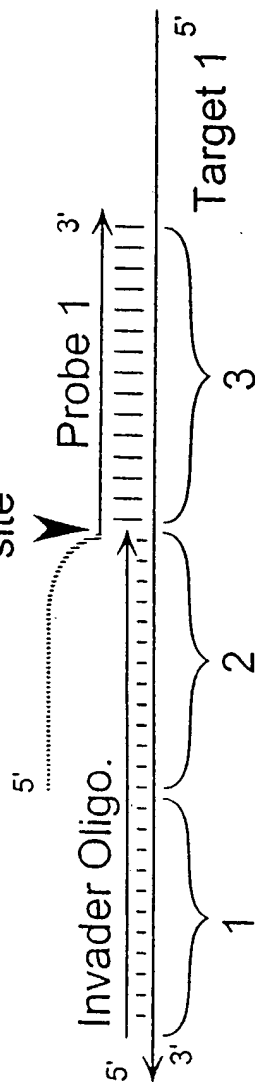


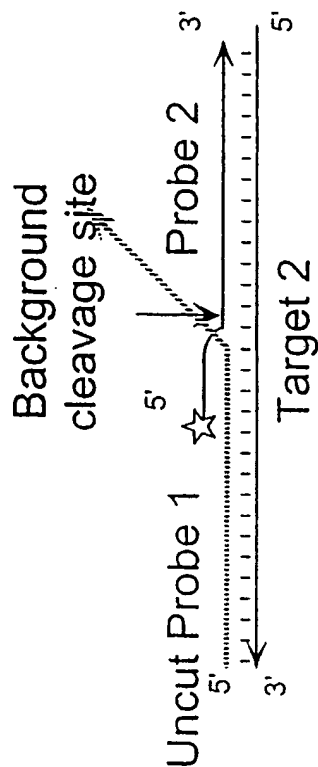
FIG. 104

FIGURE 105

Cleavage site

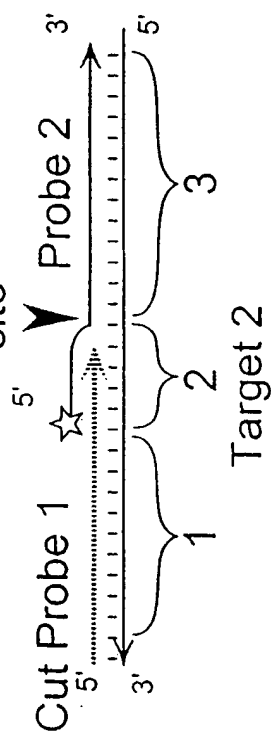


1



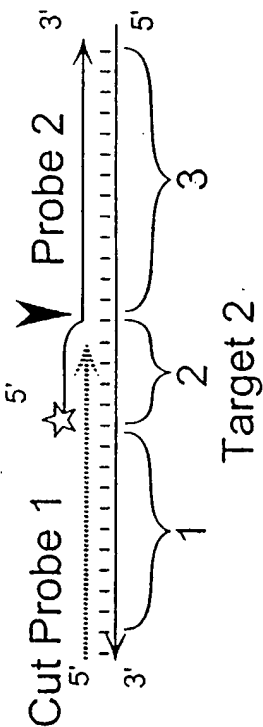
2a

Cleavage site



2b

Cleavage site



Arrested Oligo

Target 2

FIGURE 106

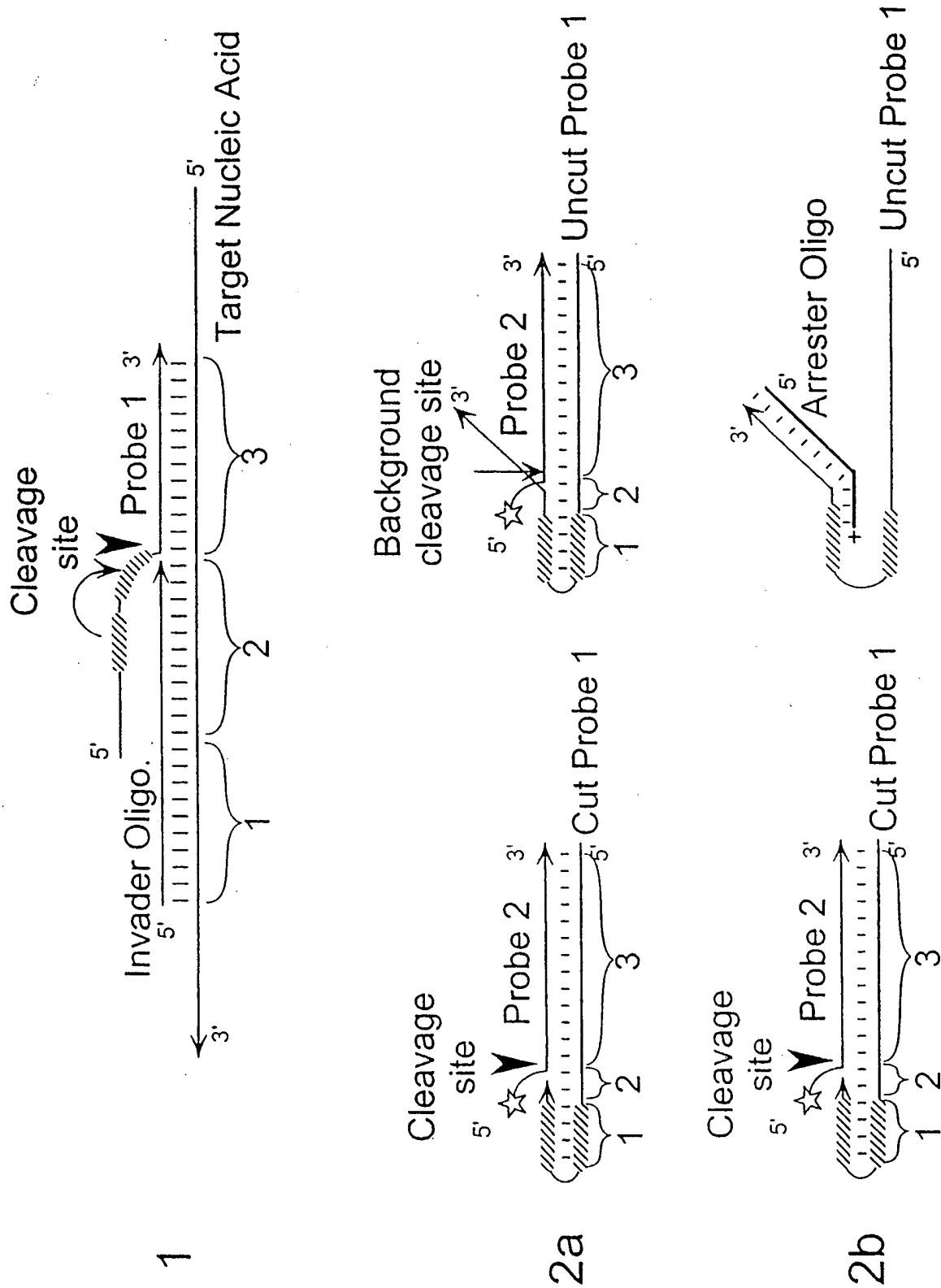


FIGURE 107

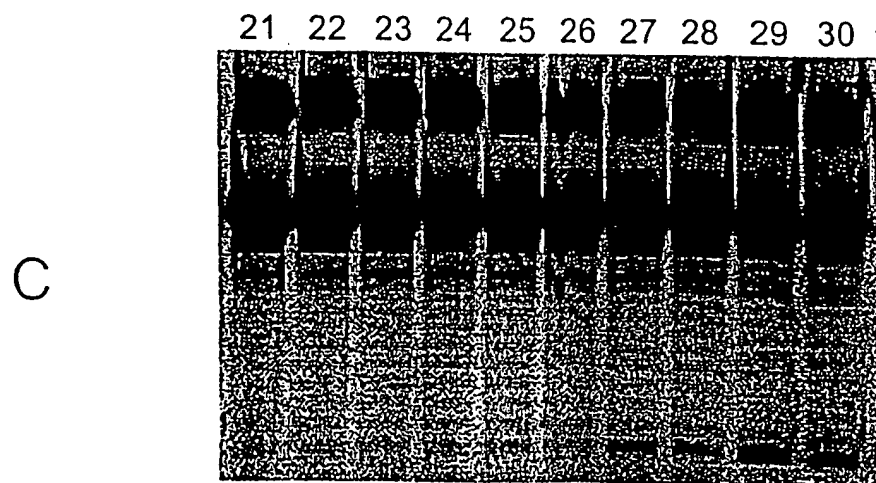
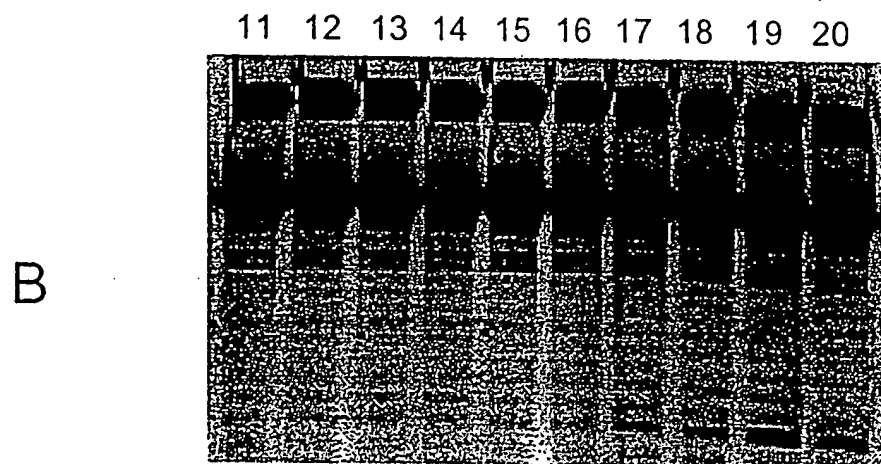
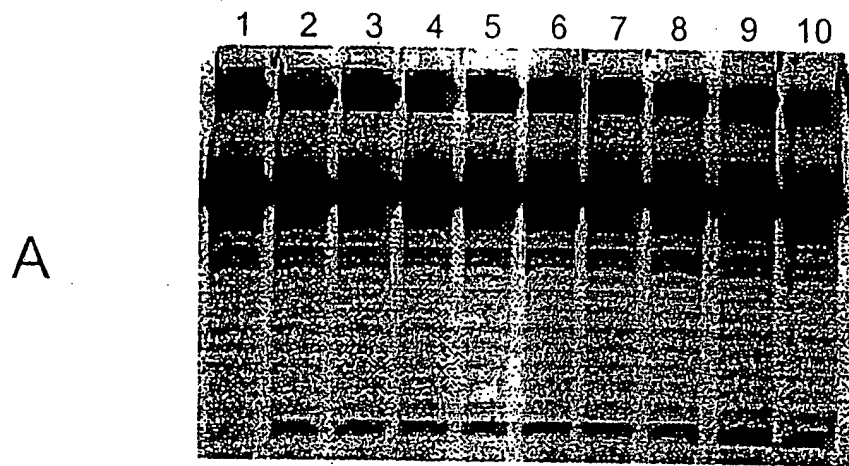


FIGURE 108A

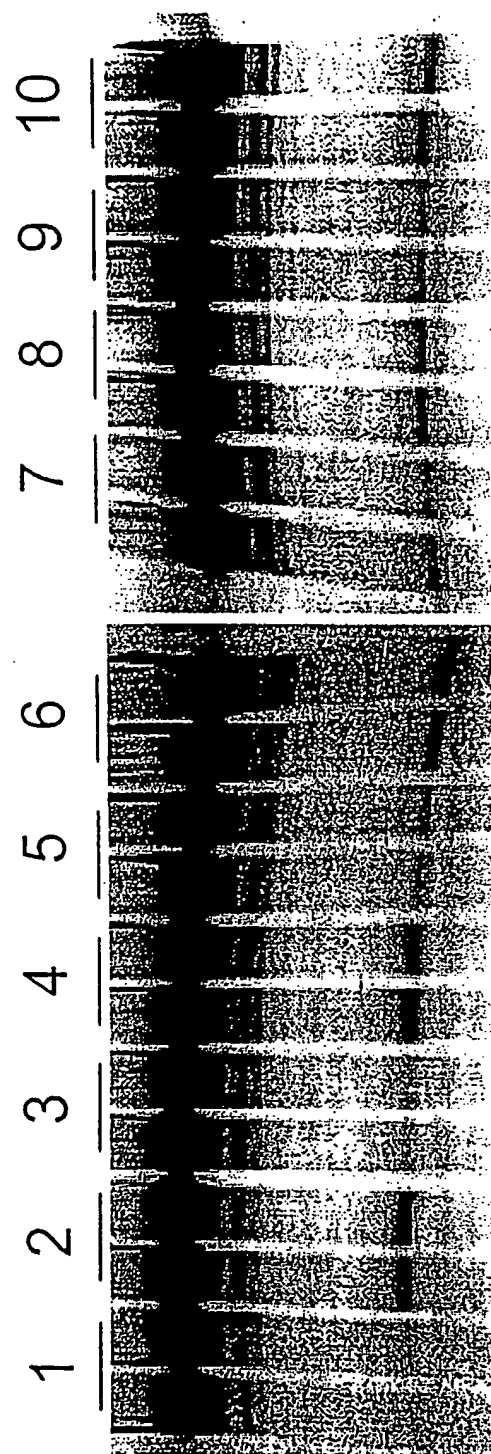


FIGURE 108B

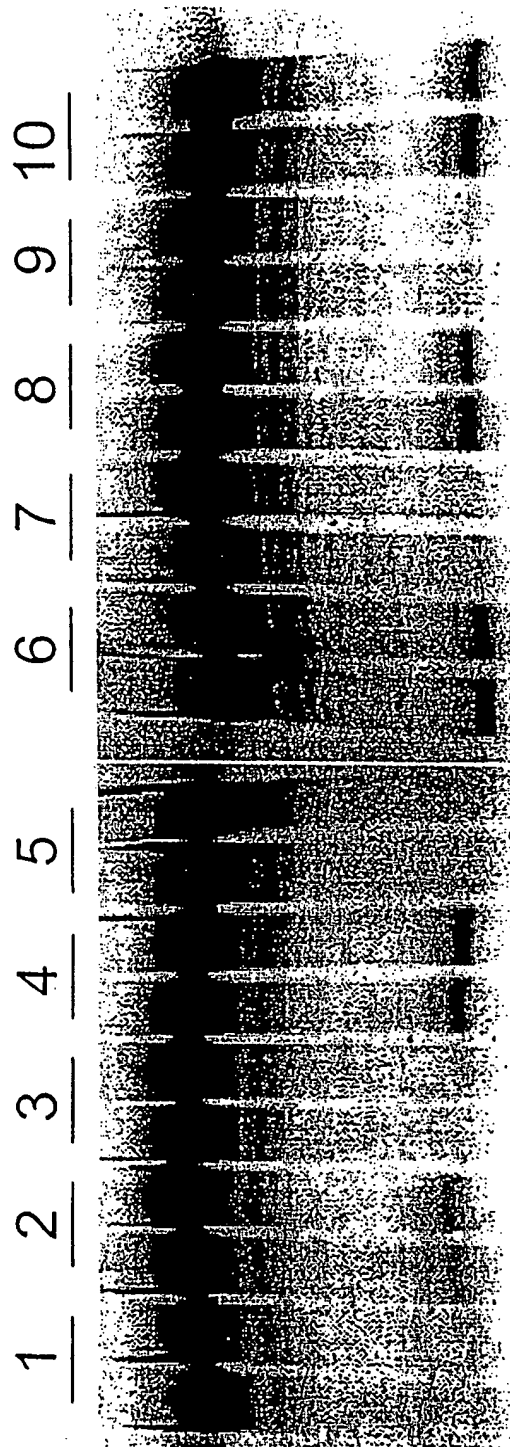
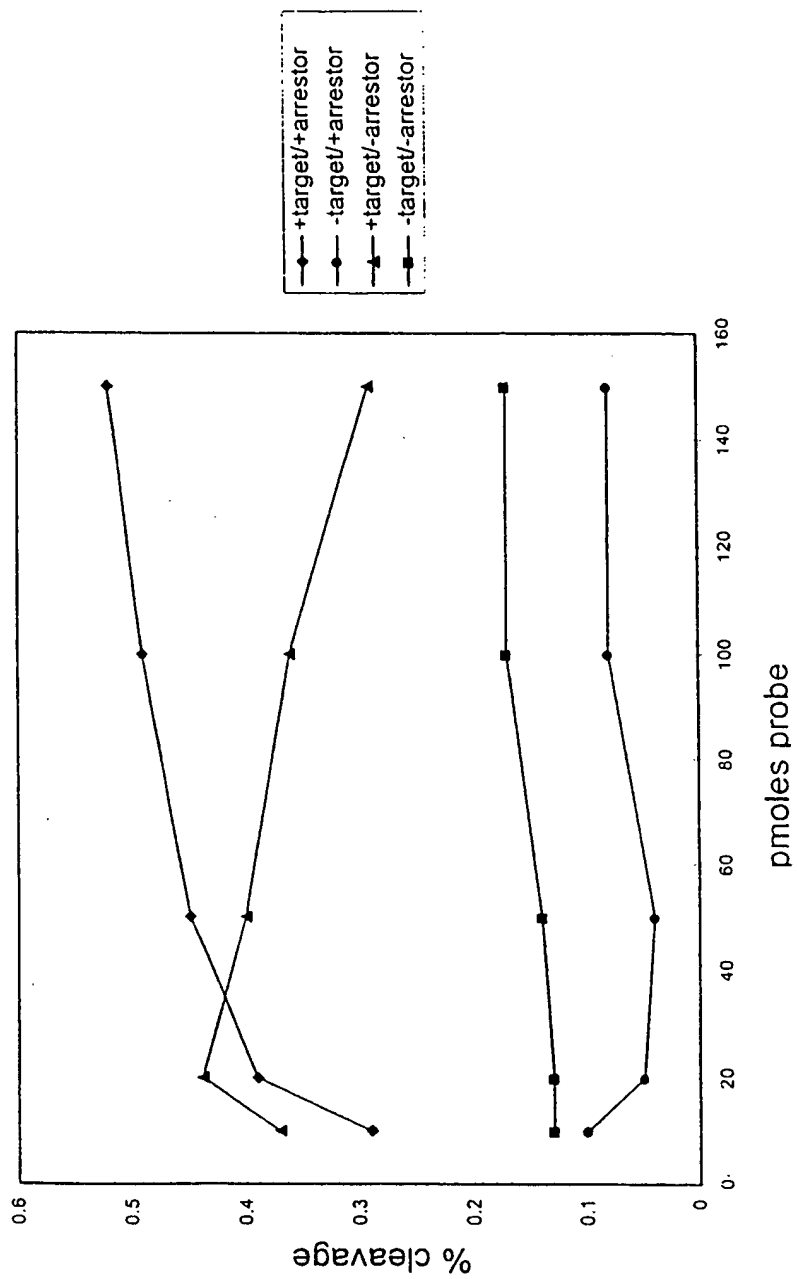


FIGURE 108C



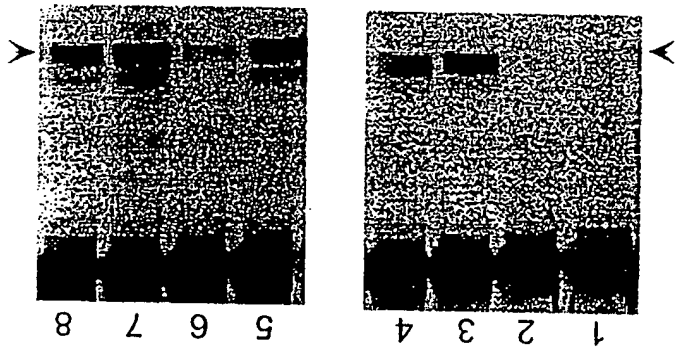


FIGURE 109A

FIGURE 109B

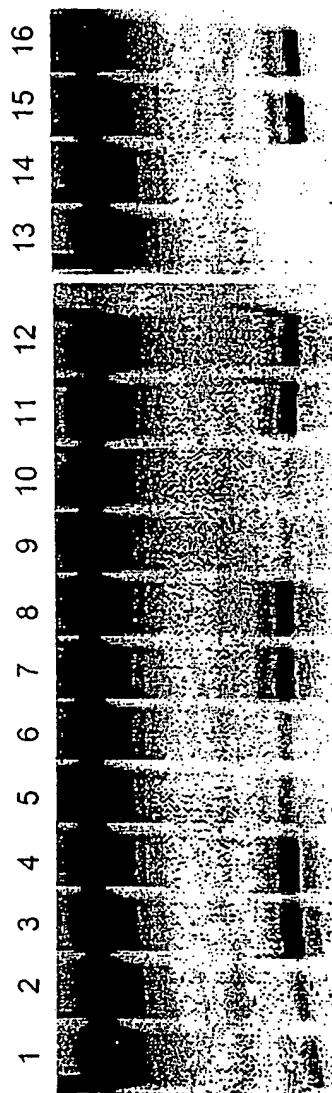


FIGURE 110A

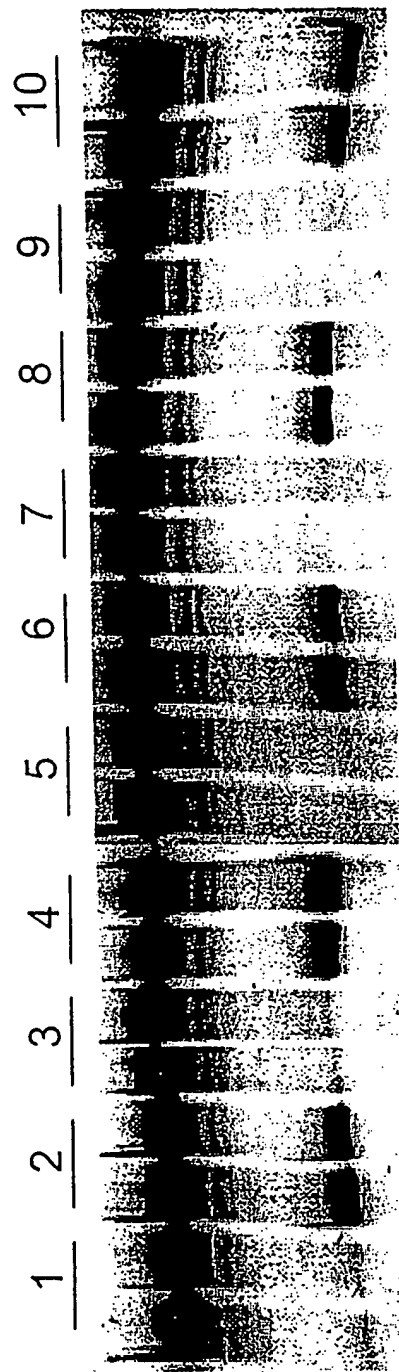


FIGURE 110B

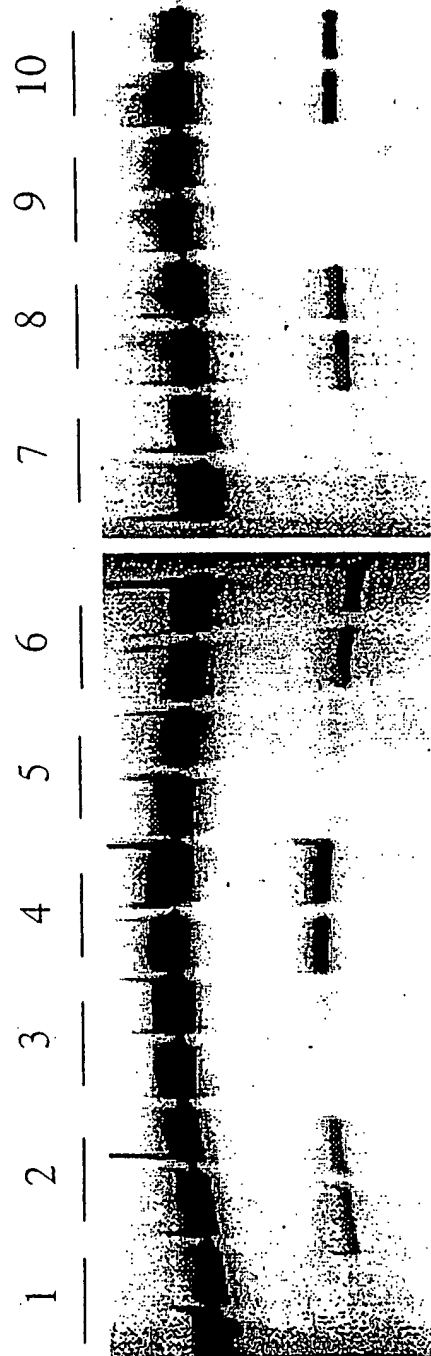


FIGURE 110C

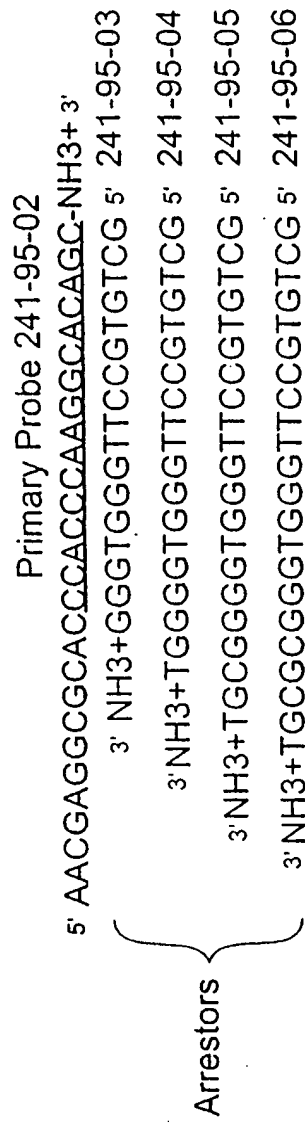


FIGURE 111

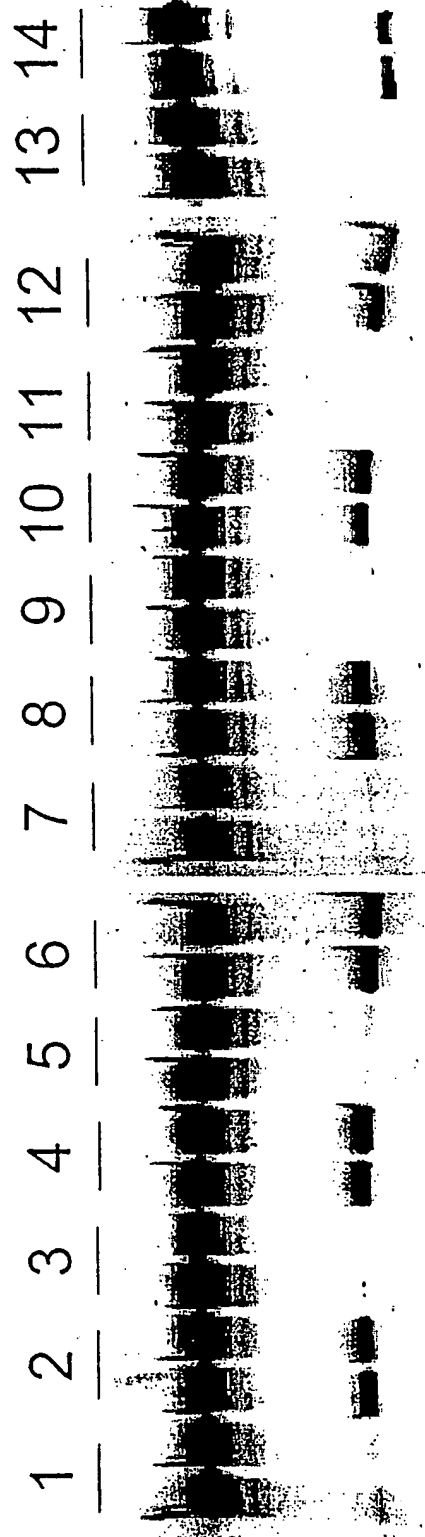


FIGURE 112

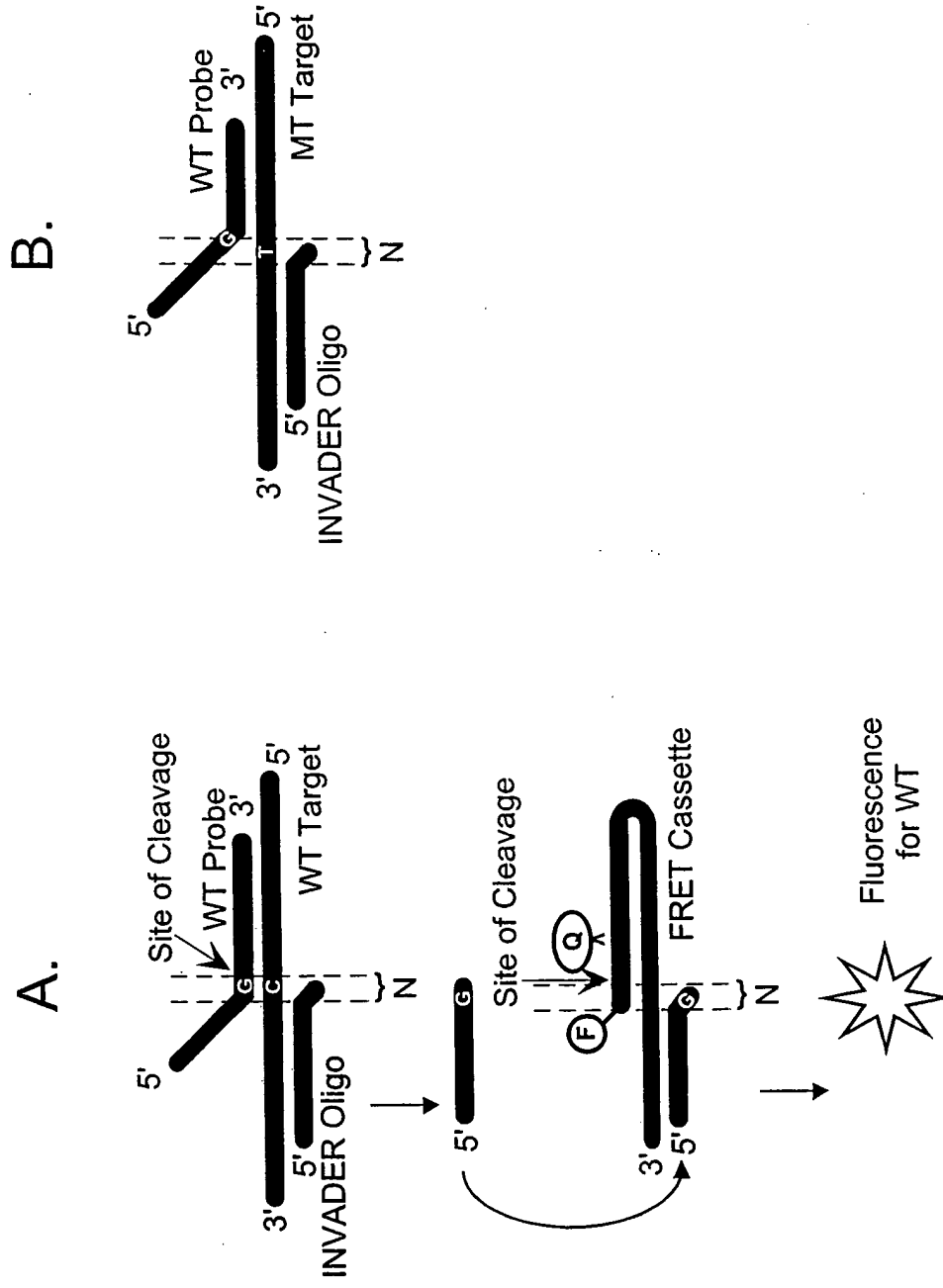


FIGURE 113A

5'-AACGAGGCGCAAGCAGTCCTCCATGT
 5'-CGGTACTGCACGAGGCGCCGCT
 3'-GAGCGCGCCATGACGTGGTCCGCGCGGTGCAGGAGGTACAGGCGCGGTC-5'

(F) (Cy3)
 CCTCGTCTCGGT T
 AACGAGGCGCACG
 3'-CTTCTCCGCGTGGGAGCAGAGCCT T

FIGURE 113B

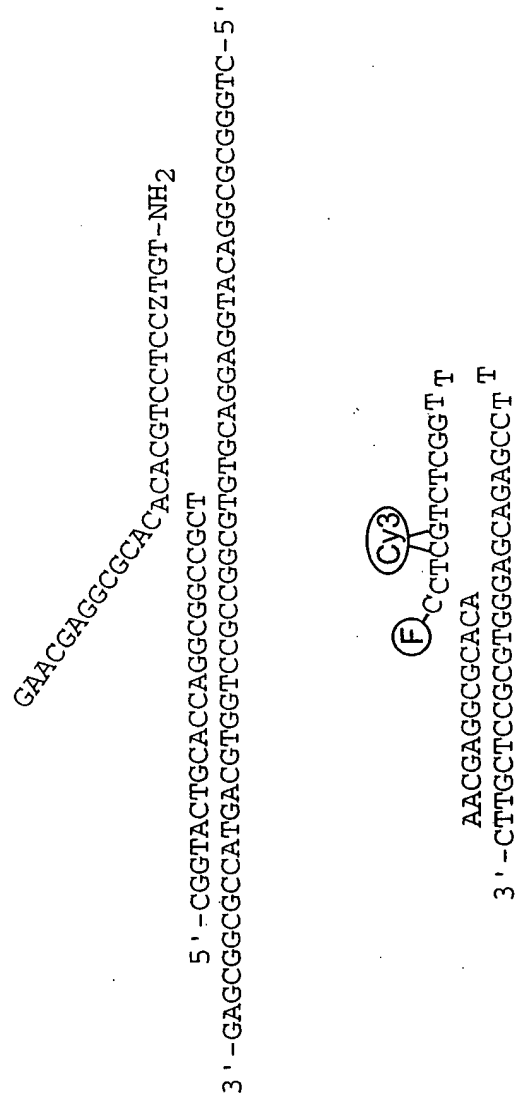


FIGURE 113C

5'-AACGAGGCGCACGCTTCTGCAGGTCATC
5'-CCCCGGCCTGGTACACTGCCAGGCT
3'-AGCGCCGGGGCCGACCATGTGACGGTCCGCGAAGACGTCCAGTAGCCGTAGCGC-5'

(F) (Cy3) CCTCGTCTCGG^T
AACGAGGCGCACG
3'-CTTGCTCCGCGTGGGAGCAGAGCCT^T

FIGURE 113D

5'-AACGAGGCGCACTTCTGCZGGTCATC
 5'-CCCCGGCCTGGTACACTGCCAGGCT
 3'-AGCGCCCGGGCCGACCATGTGACGGTCCGTGAAGACGTCCAGTAGCCGTAGCGC-5'

AACGAGGCGCACA
 3'-CTTGCTCCGCGTGGGAGCAGAGCCT T
 (F) CCTCGTCTCGG^T T
 (Cy3)

FIGURE 114A

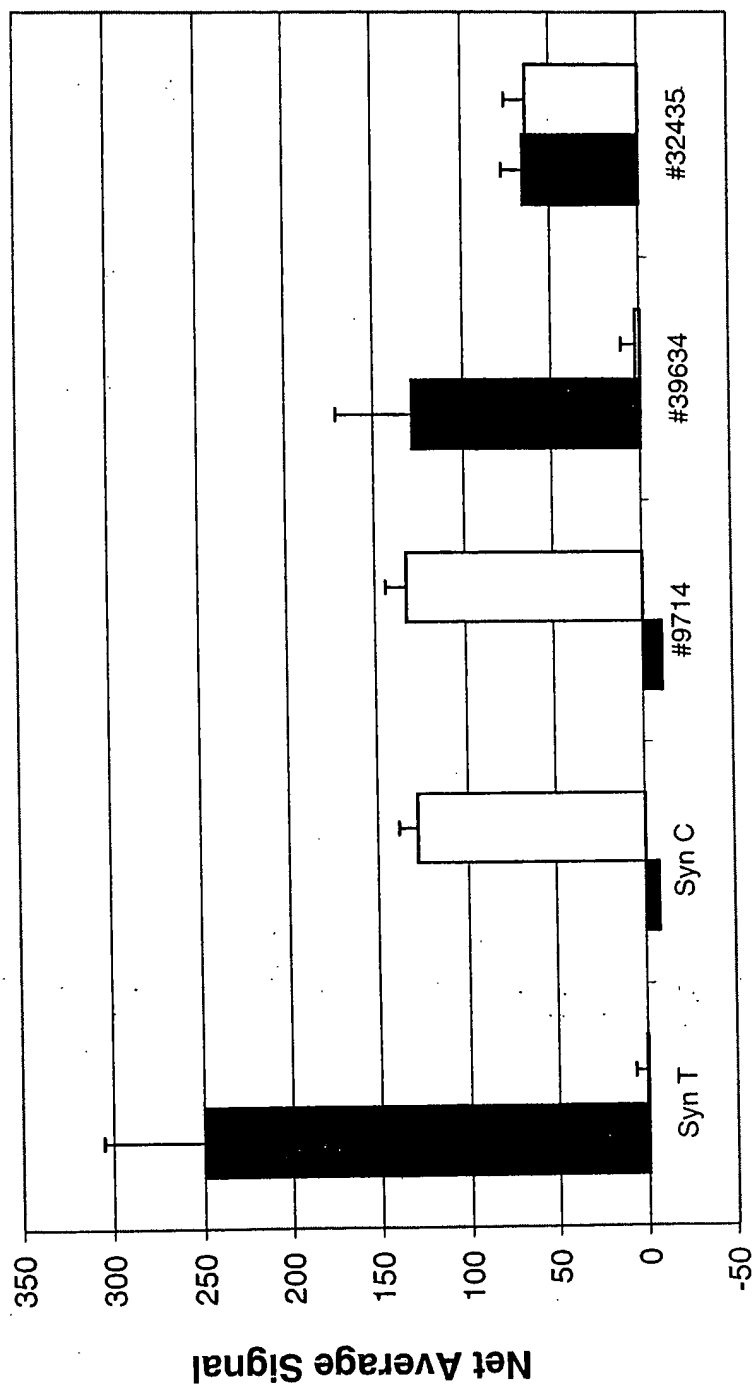


FIGURE 114B

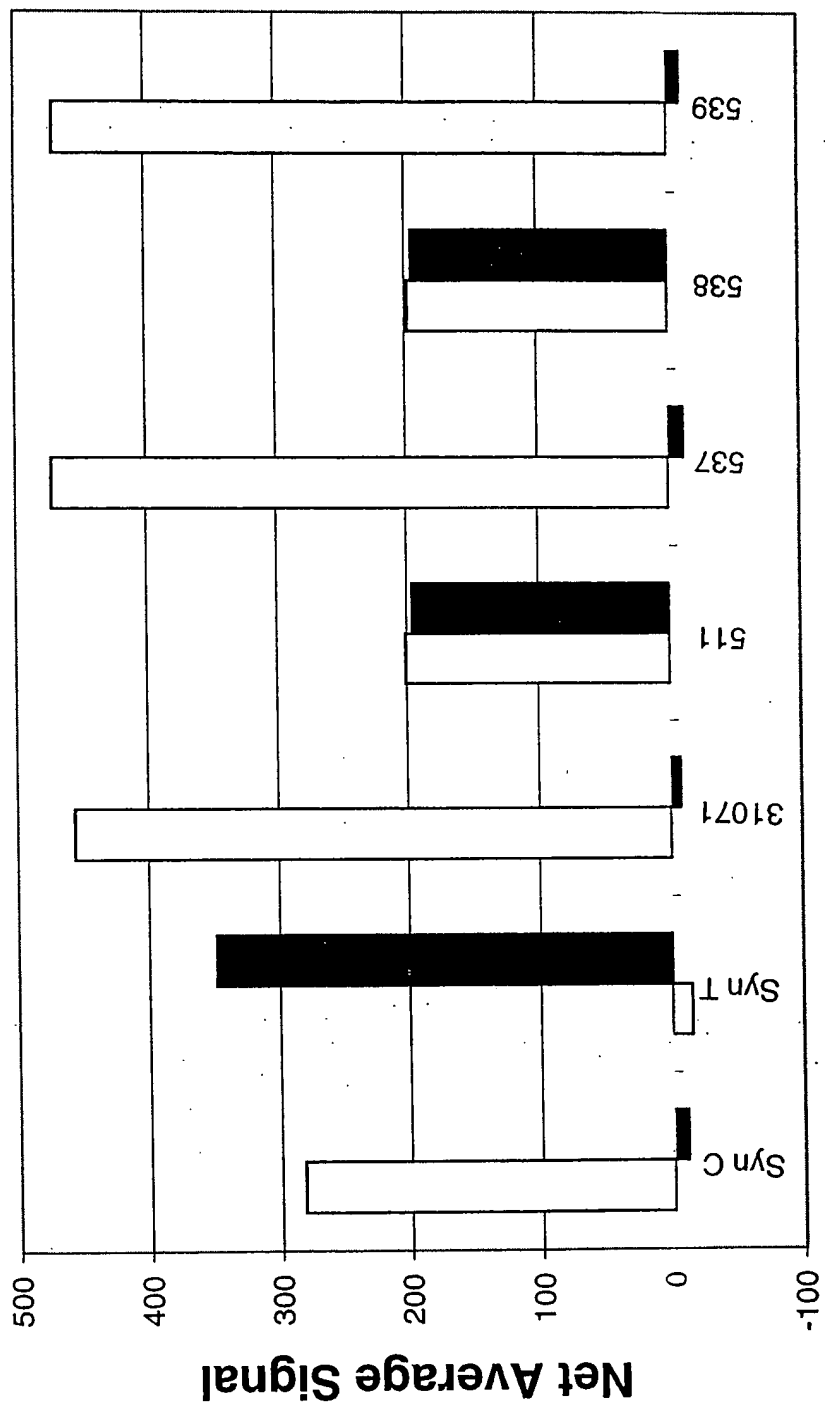


FIGURE 115A

5'-AACGAACGGCAGGCCAGGTGGAGCATT-3'
 5'-CCCCCTGGGGAAGAGCAGAGATATACGTC
 3'-GACCCCTTCTCGTCTCTATATGCACGGTCCACCTCGTGG-5'

AACGAACGGCAGG
UUUGCTTGGCGTTCGAGG-CAGAGCC₁₁
 (F) CTCCTGTCTCGGT_T
 (CY3)

FIGURE 115B

5'-AACGAACGCGCAGACCAGGTGGAGCAC-3'
5'-CCCCTGGGGAAGAGCAGAGATATACGTC
3'-GACCCCTTCTCGTCTCTATATGCATGGTCCACCCTCGTGG-5'

(F) (CY3)
CTCC GTCTCGG^T
AACGAACGCGCAGA
UUUGCTTGGCGGTCGAGG-CAGAGCC^T

FIGURE 115C

5'-AAGCAGCAGCACGATCATAGAACACGAACAGTTT-3'
 5'-GGGCTCCACACGCGGCGACTCTCATTT
 3'-GCCCCGAGGTGTGCCGCTGAGAGTACTAGTATCTTGTGCTTGTCTGA-5'

AAGCAGCAGCAGC
 (F) ACGC GTC TCCGCTT
 (CY3)
UUUCGTGCGTCGTGTGCG-CAGAGCCCTT

FIGURE 115D

5'-AAGCAGCAGCACCATCATAGAACACGAGTTT-3'
5'-GGGCTCCACACGGCGACTCTCATTT
3'-GCCCCGAGGTGTGCCGCTGAGAGTAGTAGTATCTTGTGCTTGTCTCGA-5'

Ⓕ ACGC GTCTCGGTT
AAGCAGCAGCACCC
UUUCGTGCGTCGTGTGCG-CAGAGCCCT

FIGURE 116

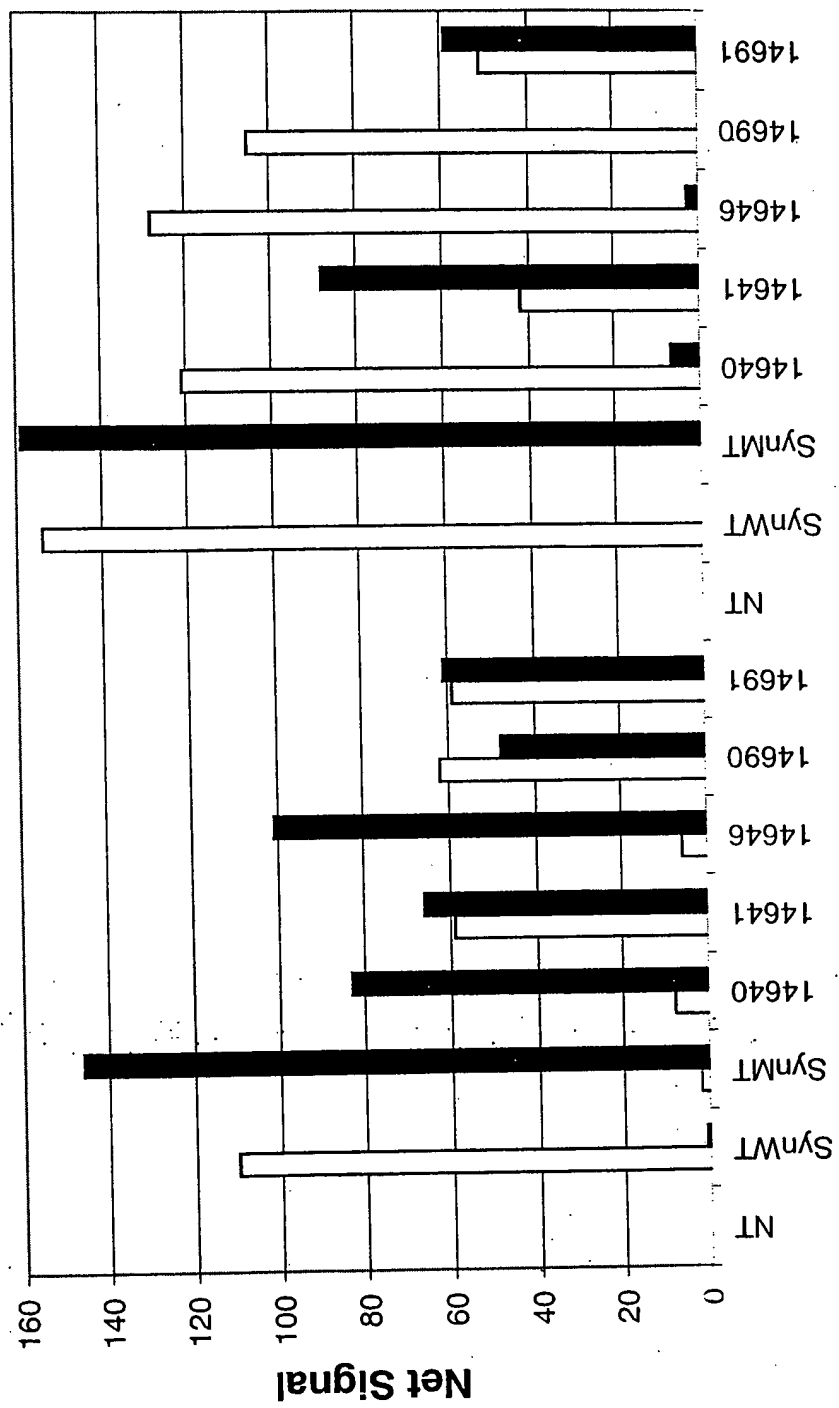


FIGURE 117A

5'-AACGAGGCGCACGCTCCCGCAGACAC-3'
 5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC
 3'-GGAGTTTCTTTTCGACGCACACTACTTTAGCCGAGGGCGTCTGTGGAAG-5'

5'-AACGAGGCGCACG
 3'-NH₂-TTTGCTCCGCGTGGGAGCAGAGCC-T
 (F) (Cy3)

FIGURE 117B

5'-AACGAGGCGCACTCCCGCAGACACC-3'
 5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC
 3'-GGAGTTTCTTTTCGACGCACTACTTTAGCTGAGGGCGTCTGTGGAAG-5'

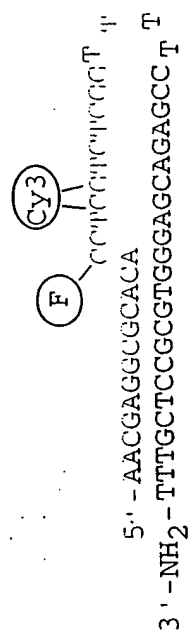


FIGURE 118

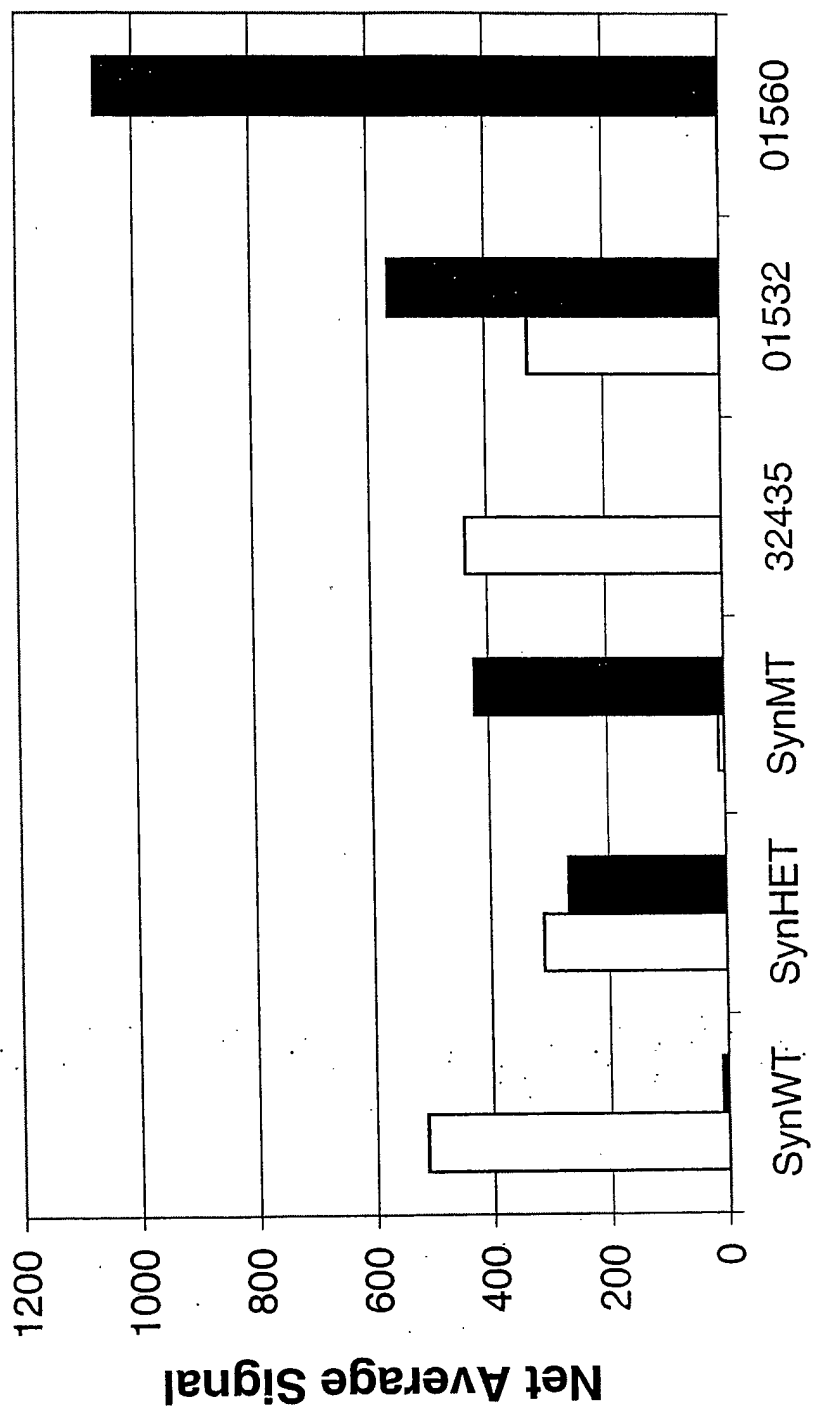


FIGURE 119A

5'-AACGAGGCGCACGAGCCTCAATGCTCCC-NH₂-3'
5'-TATGGTTCCCAATAAAAGTGACTCTCAGCT
3'-TTGATACCAAGGGTTATTTTCACTGAGAGTCGCTCGGAGTTACGAGGGGTCA-5'

5'-AACGAGGCGCACG
3'-NH₂-TTTGCTCCCGGTGGGAGCAGAGCC-TT

(F) (Cy3)

CCTCGTCTCGGT T

FIGURE 119B

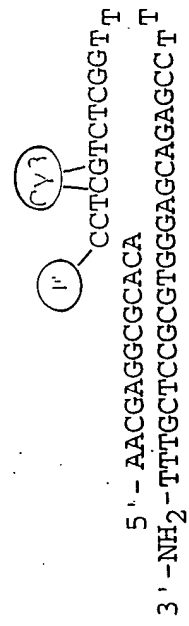
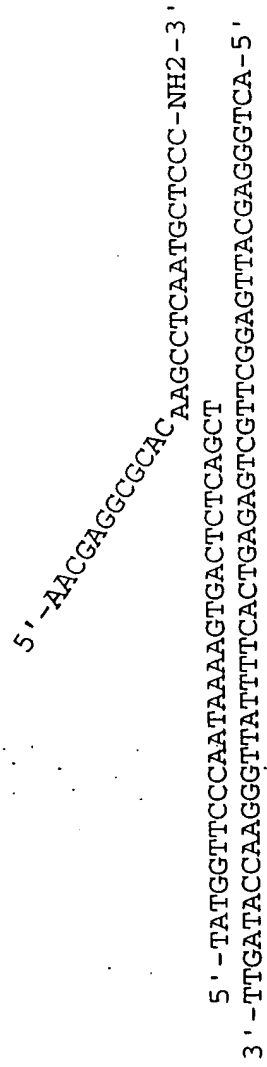


FIGURE 120

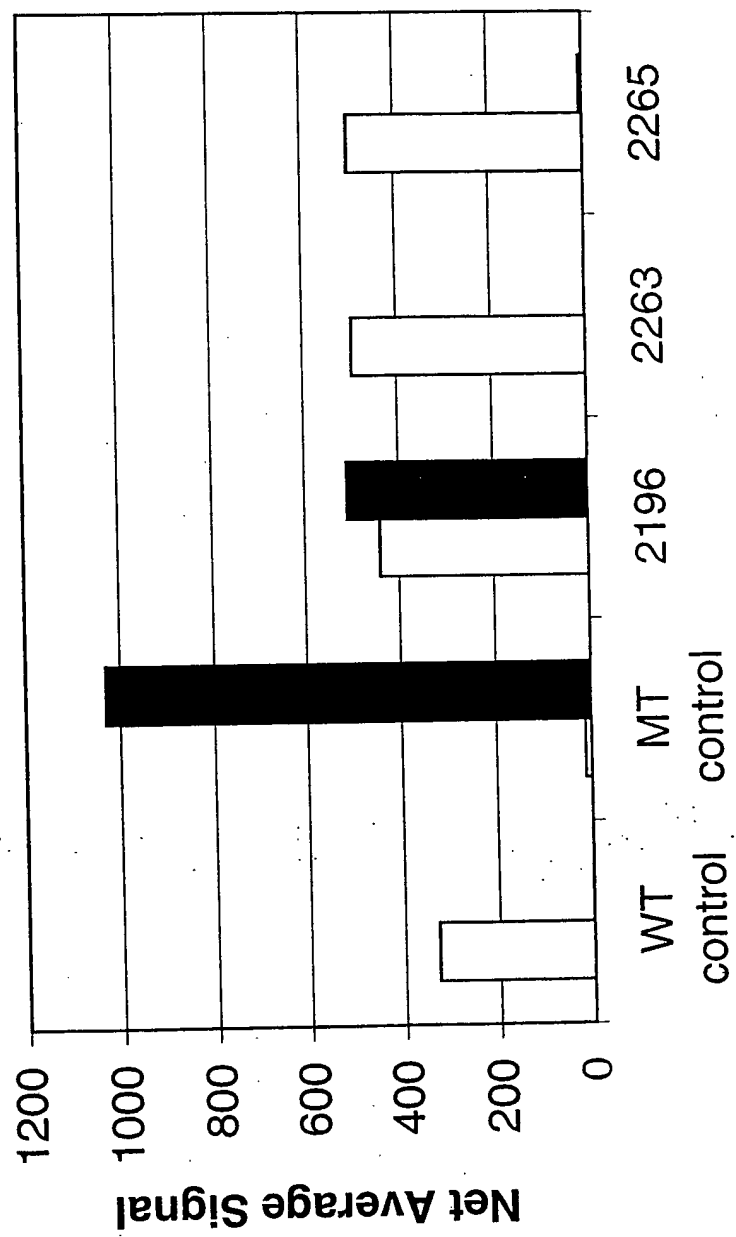


FIGURE 121A

5'-AAGCAGCGAGCAGCGTACAAACCCTTTCTCTAGACAAA
5'-AGATGCCCATTTCTCCAGACCTCAGCCC
3'-GTCTACGGGTAAAGAGGTCTGGAGTCGGCATGTTGGGAAAGAGATCTGAAGT-5'

(F) (CY3) CTCC GTCTCGG^T
AAGCAGCGAGCAGC
UUUCGTCGTCGTGGAGG CAGAGCC^T

FIGURE 121B

5'-AAGCAGCAGCA CAGGAACCCCTGTGACAT-3'
 5'-CCATCCAGGGAAGAGTGGCCCTGTTT
 3'-GGGTAGGTCCCTTCTCACCGGACAATCCTTGGGACACTGTAAAGTTT-5'

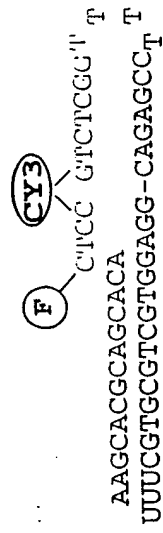


FIGURE 122

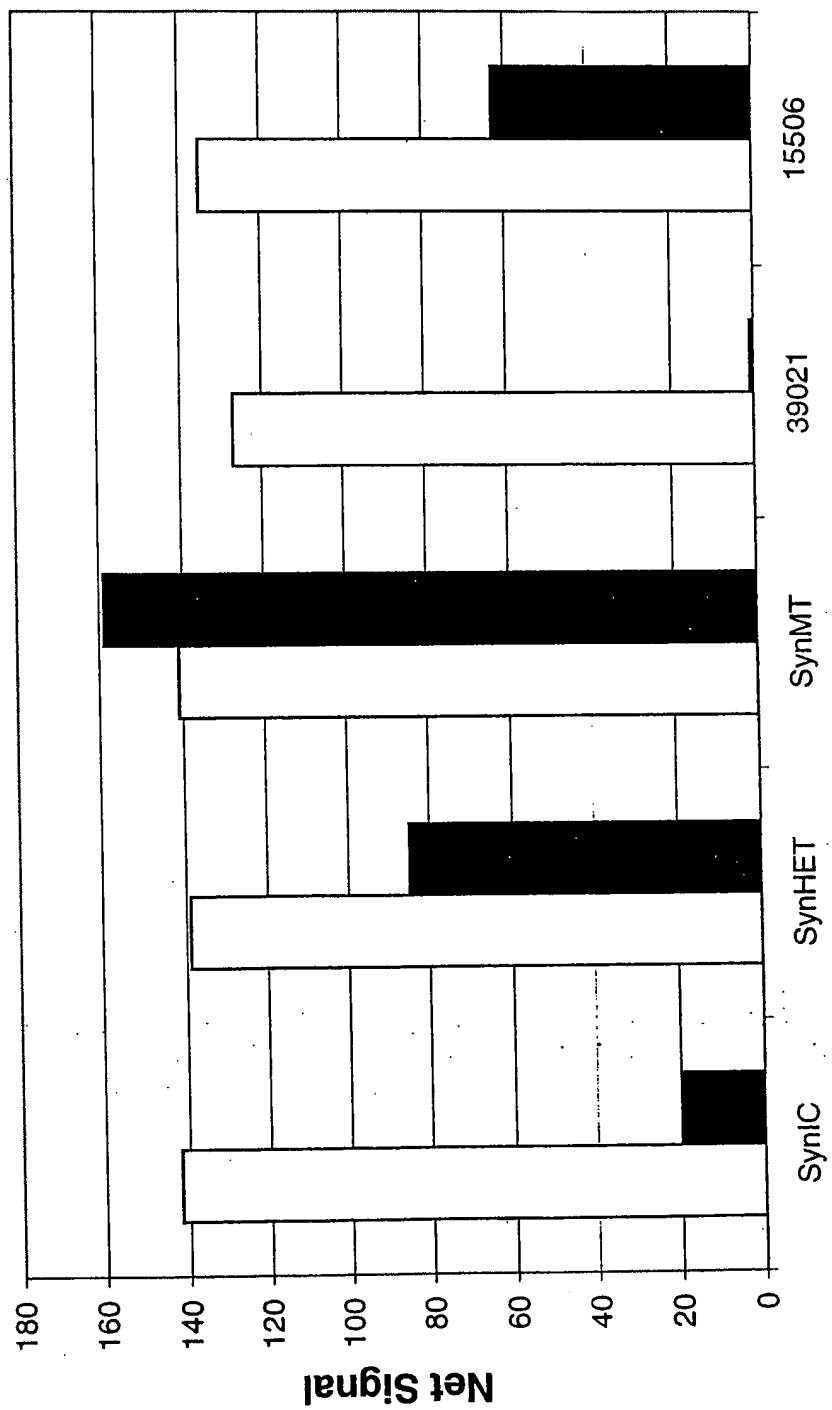


FIGURE 123A

5' - AACGAGGCGCAC CCATGCCCCCTCAAAAC
 5' - GACCCGTGGAGGCTGAACCCCGTCCA
 3' - ATCC'TGGGACCTCCGACTTGGGGCAGGGGTACGGGGAGTTTGGAT-5'

5' - AACGAGGCGCACC
 3' - NH₂ - TTTGCTCCCGTGGGAGCAGAGCC T

F
 CY3

FIGURE 123B

5'-AACGAGGCGC¹TCATGCCCCCTCAAAAC
5'-GACCCCTGGAGGCTGAACCCCGTCCA
3'-ATCCTGGGACCTCCGACTTGGGCGAGGAGTACGGGGAGTTTGGAT-5'

5'-AACGAGGCGCACT
3'-NH₂-TTTGCTCCGCGTGGGAGCAGAGCC T
F
CY3
CCTCGTCTCGGT T

FIGURE 124

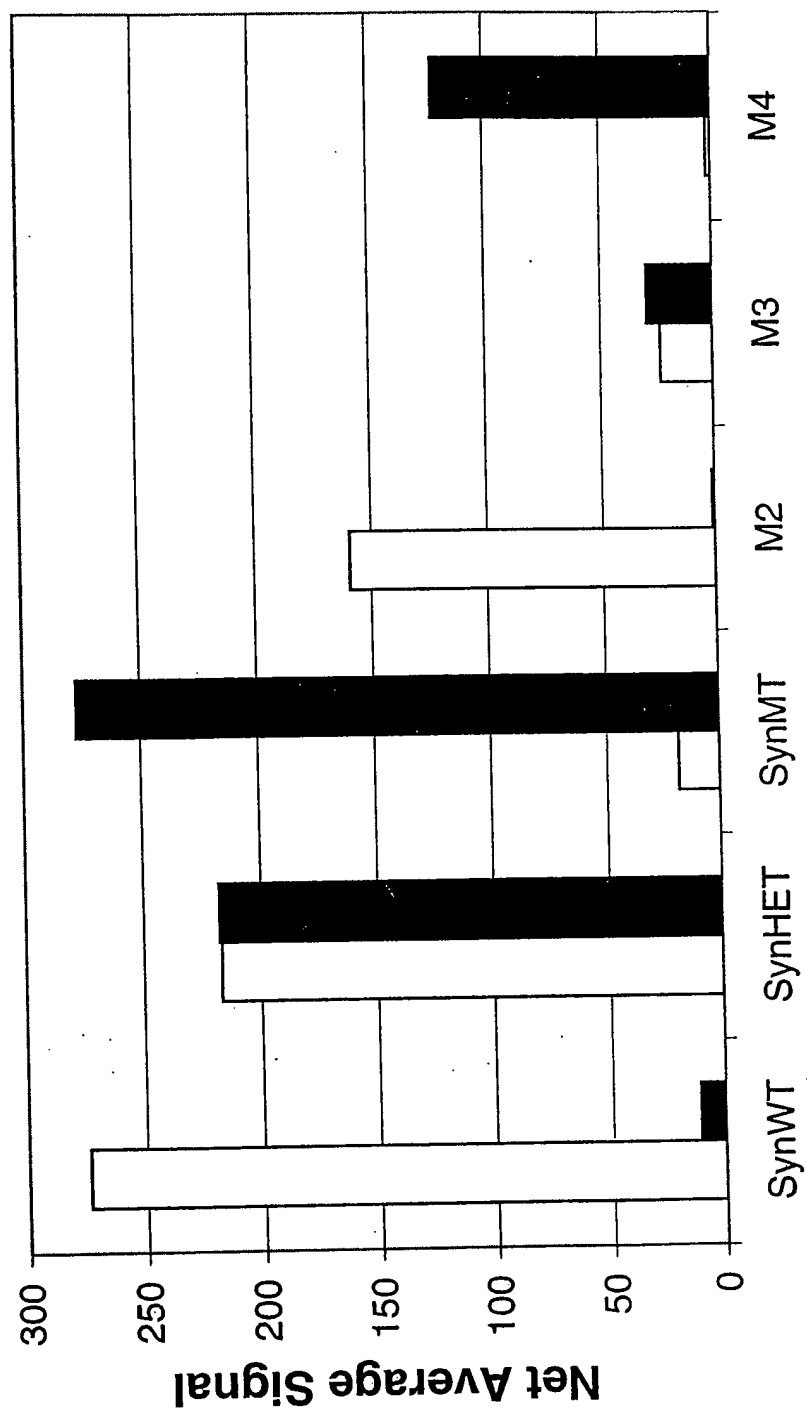


FIGURE 125A

5' - AACGAGGCGCAC GAGGAATACAGGTATTTGTC - NH₃
 5' - TAATCTGTAAGAGCAGATCCCTGGACAGGCC
 3' - AGATTAGACATTCTCGTCTAGGGACCTGTCCGCTCCTTATGTCCATAAACACAGGAA - 5'

5' - AACGAGGCGCACG
 3' - NH₂ - TTTGCTCCGCGTGGGAGCAGAGCC T

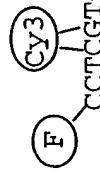


FIGURE 125B

AACGAGGCGCAC AAGGAATACAGGTATTTTGTGTC-NH3
 5'- TAATCTGTAAGAGCAGATCCCCTGGACAGRCC
 3'- AGATTAGACATTCTCGTCTAGGGACCTGTCCGTTCCCTTATGTCCATAAAACAGGAA-5'

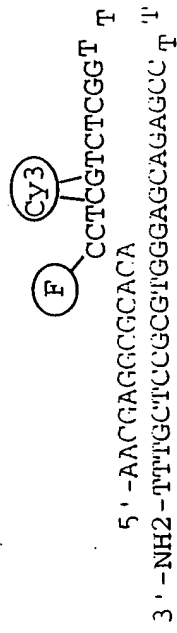


FIGURE 126

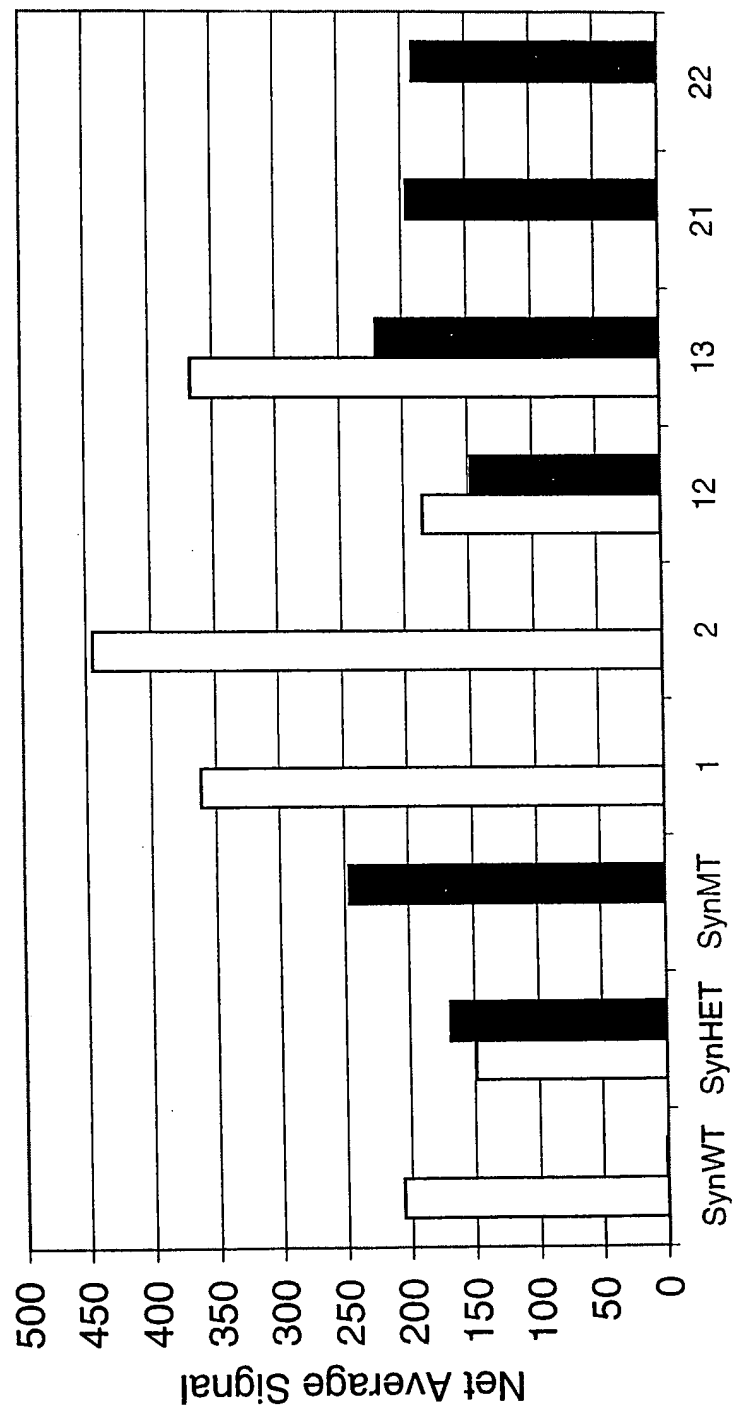


FIGURE 127A

5' - GCGCCGAGG TCTTGGGGTGGTTACAAG-NH₂-3'
 5' - GGTAAGGTTGGCAAAAAGATAAC
 CCATTCCAAACCGTTTCTATTAGAACCCCAATGTTC-5'

(F) (CY3)
 5' - GCGCCGAGGT
 B - GCGCGGCTCCAGAGTCAGAGCC T

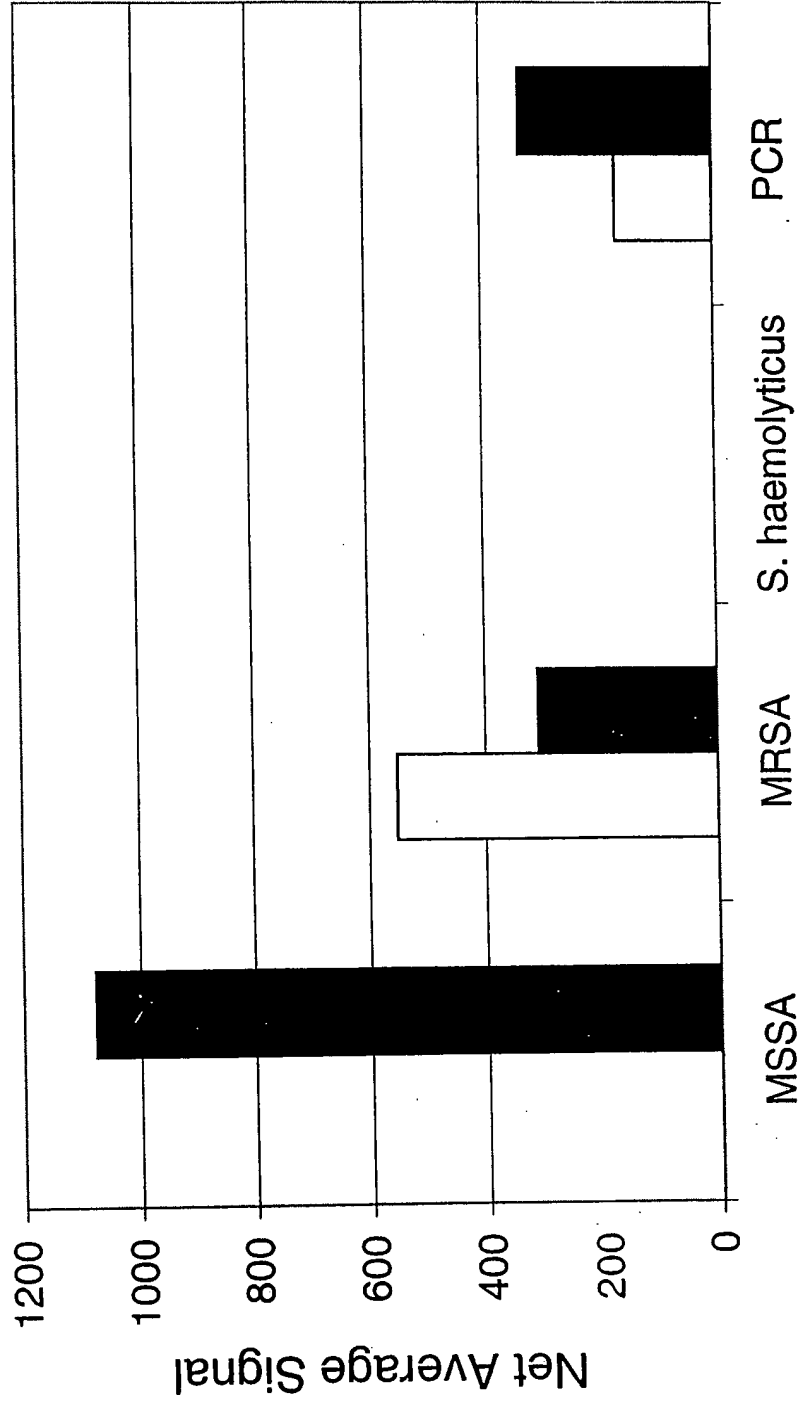
FIGURE 127B

5'-CGCGCCGAGGACACCTTTTATAGGGTGCTTTGT-NH₂-3'
5'-CACTTGCTTCAGGACCATAATTTCTCTCTC
GTGAACGAAGTCCTGGTATAAAGAGAGATGTGGAAAAATCCACGAAACA-5'

5'-CGCGCCGAGGA
B-GCGGGCTCCAGAGTCAGAGCCTT

(F) TCTC GTCTCGG^T T
(CY3)

FIGURE 128



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